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                                       GGAGCTACTTGTTCTCGGTGTCTTAGATTGGAGGCTAAGATCAGTAACACCACTTTGCTT
                                                                             TCTTGATCTCCAGGTTGAAGGTGCAAAATATATTTTCGAGCCGAAAACAATCCGAAGAAT
                                                                                         CTTGGACCTTCAGATAGAAGGTGCCAAGTACATATTTGAGCCGAGAACAATTCGTAGGAT
                                                                                                                               CTTATCTGTAGCATGCTTGTCTTTAGCTGCTAAAATGGAGGAAACCCTTATTCCTTCTAT
                                                                                                                                                                               TCTGGATCGTTTCATCTATTGCCGTGGCTTCCCGGTGGCAAATGGGTGGCCCTTGCAACT
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                          GGAGTTTCTTGTGCTTAGTGTTTTTGGATTGGAGACTAAGATCCGTTACACCGTTTAGCTT
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Sequence 4 from
A85060
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PALENT: WO 9842851-A 4 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); U
Location/Qualifiers
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/db_xref="taxon:4233"
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Pred. No. 1.3e-81;
0; Mismatches 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of E
Cambridge, Tennis Court Road, Cambridge, CB2 1QT,
revised by [3]
3 (bases 1 to 1951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A. A family of cyclin D homologs from plants differentially by growth regulators and containing the conserved retinob protein interaction motif plant Cell 7 (1), 85-103 (1995) 95210930
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A.thaliana mRNA for cyclin
X83369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; cdre eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Ecambridge, Tennis Court Road, Cambridge, CB2 10T On Mar 28, 1998 this sequence version replaced gliocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyclin; cyclin delta-1.
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                           /codon_start=1
/product="cyclin_delta-1"
/protein_id="cas8285.1"
/protein_id="cas8285.1"
/protein_id="cas8285.1"
/db_xref="gi:2995130"
/db_xref="gi:2995130"
/db_xref="gi:2995130"
/db_xref="SWISS-PROT:P42751"
/db_xref="SWISS-PROT:P42751"
/translation="MRSYRFSDYLMHSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEV
DSWPGDSTACFIEDERHFYDGHDYLSRFQTRSLDASAREDSVAMILKVQAYYNKQPLT
AYLAVMYMDRFLYARRLPETSGWPMOLLAVACLSLAAKMEEILVPSLEDFOVAGVKYL
FEAKTIKRMELLVLSVLDMRLRSVTPFDFISFFAYKIDFSGFFIGFFISHATEITLSN
IKEASFLEYMPSSIAAAAICVANELPSLSSVVNPHESPHTWCDGLSKKKIVRCYRI
IKEASFLEYMPSSIAAAAICVANELPSLSSVVNPHESPHTWCDGLSKKKIVRCYRI
IKEASFLEYMPSSIAAAAICVANELPSLSSVVNPHESPHTWCDGLSKKKIVRCYRI
IKEASFLEYMPSSIAAAAICVANELPSLSSVVNPHESPHTWCDGLSKKKINGVSMVGDETSTS
                                                                                                                                                                                                                                                                                                  /variety="ecotype Landsberg
/db_xref="taxon:3702"
                                                                                                                                                                                                                                104. .1111
                                                                                                                                                                                                                                           /dev_stage="seedlings,
                                                                                                                                                                                                                                                               /tissue_type="whole seedlings"
/clone_lib="pFL61"
                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
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                               CAAGGCCAAGTGATGAATCCTCTT
                                                                                                                                                                                             AAGAAAAAGTAATAGGGTGCTACCAGTTGATGCAAGAGCTTGTGATTAACAATAACCAAC 1010
                                                                                                                                                                                                                                         CTCTATCCTCTGTTGTCAATCCCCACGAGAGCCCTGAGACTTGGTGTGACGGATTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                       TCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAGAGGCTAGCTTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGGCCTGGTGATTCTATCGCTTGTTTTATCGAAGACGAGCGTCACTTCGTTCCTGGAC
                                                                                                 TAAATACACCAAAAGTGATAGCAAAGCTTCGAGTGAGTGTAAGGGCATCATCGACGTTAA
                                                                                                                                  GGAAACTCCCCTTACTAAAAGTGTTGCCGCAGCTGCGAGTAA---CAACTCGGACCCGAA 1067
                                                                                                                                                                                                                                                                                                               AGTACTGGCCATCGAGTATAGCTGCAGCCGCGATTCTCTGTGTAGCGAACGAGTTACCTT
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                                                                                                                                                                     AAGAGAAGATAGTGAGATGCTATAGACTGATGAAAGCGATGGCCATCGAGAATAACCGGT
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/note="pest motif, p
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167. .181
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AUTHORS
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TITLE
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Best Local Similarity
Matches 548; Conserv
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                                                                                                                CTTGTCATTAGCTGCTAAGATGGAGGAATCTCTGGTTCCTTTTTTGGATCTTCAGGT
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                                                                                                                                                                                                                                                                                                GTACTATGGCTTTCAGCCTTTGACGGCGTACCTCGCCGTCAACTATATGGATCGGTTTTT
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                                           GGAAGGAGCAAACTTTATTTTTGAACCAAGAATATCCAAAGAATGGAGCTTCTTGTGCT
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Antirrhinum majus mRNA
AJ250396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaudin, V., Lunness, P., Fobert, P., Towers, M., Riou-Khamlichi, C., Murray, J., Coen, E. and Doonan, J.H.
The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ250396.1 GI:6448
CycDl gene; cyclin
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1 (bases 1 to 1162)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="cyclin d1"
/product="cyclin d1"
/product="cyclin d1"
/protein_id="GAB61221.1"
/db_xref="G1"6448480"
/db_xref="G1"6448480"
/translation="MSISCSDCFSDLLCGEDSNIIFSGGGDDLPEYTSDVESIPTDVD
ESIAGLLEDERDLAGVNSSSSNOSVDSSTRTESTAWILKVQRYYGFQPLTAYIAVSYF
DRFLNAHHLPKLNGWPWQLLSVACLSLAKKEESLYPSLLDLCYBCANFIFEPRNIOR
MELVLRVLDWRLRSISPFCYLSFFALKIDPTGTYTGFITSRAKEIILSTVQETSLIE
YRPSCIAAATMLSSANDLPKFSFITAGHAEAWGDGLHKDNIASCIKLIGVESNNRPK
KQPKVLPQLRVMTRASLASSESSSSTSSSSPSYKRRKLNNSSRADDDKESSDYGV"
a 268 c 246 g 315 t
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/db_xref="taxon:4151"
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                            AGGTACACGCGTACTATGGCTTTCAGCCTTTGACGGCGTACCTCGCCGTCAACTATATGG
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PATENT: WO 9842851-A 2 01-CTT-1998;
URRAY JAMES AUGUSTUS HENRY (GB); UI
LOCATION/QUALIFIERS
1. 1679
                                                                                                                                                                                                                                                                                                                               common tobacco.

Nicotiana tabacum

Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Nicotiana.
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Sequence 2 from Patent WO9842851.
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Pred. No. 3e-26;
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                                                                                                                                                                                                                      Direct Submission
Submitted (07-OCT-1998) Murray J.A.H., Insti
University of Cambridge, Tennis Court Road,
2 (bases 1 to 1679)
                                                                                                                                                                                                                                                                                         common tobacco.

Micotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Micotiana.

1 (bases 1 to 1679)
                                                                                                                                                        Distinct cyclin D genes show mitotic accumulation levels of transcripts in tobacco bright yellow-2 plant Physiol. 119 (1), 343-352 (1999)
                                                                                                                                                                                                Sorrell,D.A., Combettes,B., Chaubet-Gigot,N., Gigot,C. Murray,J.A.
                                                                                                                                                                                                                                                                                                                                                                          CycD3.1 gene; cyclin D3.1 protein
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AJ011893.1 GI:4160299
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                           /gene-"CycD3.1"
181. .1302
                                                    /dev_stage-"Exponentially 181. .1302
                                                                                         /organism="Nicotiana tabacum"
/db_xref="taxon:4097"
                                                                                                                   Location/Qualifiers
1. .1679
/gene="CycD3.1"
/codon_start=1
                                                                              cell_line="Bright Yellow 2 (BY-2)"
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Road, Cambridge, CB2 1QT, UK
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ACCAGTTGATGCAAGAGCTTGTGATTAACAATAACCAACGGAAACTC 1018
                                                ACTACCAAAATCAACTTCTTGGGGTTCTCAAAATTAACAAGGAGAAAGTGAATAATTGCT
                                                                                           ATCATATTATAAGGAGGCTTGGGCTAAGAAATAATATTCACTGGGAATTTCTTAGAAGAT
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/protein_id="CAA09853.1"
/protein_id="CAA09853.1"
/db_xref=="C1:4160300"
/db_xref=="C0:4160300"
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/translation="MAIEHNEOOELSQSFLLDLYCESEEEKWGDLVDDETIITPLSS
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/translation="MAIEHNEOOELSQSFLLDLYCESEEKWGDLVDDETIITPLSCARTITYTERFLISHIYOKDKPWMIOLAANTCLLAA
RVDSVEWILKUNGYYGESALTAVLALAYYEDRETLISLIKWRWNPVTPLSFLDHIIRRL
GLRNNIHWEFLARCENLLLSIMADCRFVXHDSVLAATAIMLHYIHOVEPCNSVDYQNO
LLGVLKINKEKVNNCFELISEYCSK DISHKRKYENPSHSPSGVIDPIYSSESSNDSWD
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                                                                                   AACCTCTTGTTCCATCTCTCTTGGACCTTCAGATAGAAGGTGCCAAGTACATATTTTGAGC
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                                                            AAACTCAAGTTCCTCTTCTTTTGGACTTCCAAGTGGAGGATGCAAAATATGTGTTTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUN-1998) Masami Sekine, Nara Institute of Science and Technology, Graduate School of Biological Sciences; Takayama 8916-5, Ikoma, Nara 630-0101, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only 2 (bases 1 to
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LPLPLLEQDLEWEDEELLSLETKEKETISNFETIKTDPLLCLSKEKEWWEILKVNAHY
GFSTFTAILANIYFDRFLSSLHFWKKFENDLLDAVTCLSLAAKVEETQVPLLLDGQV
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RILLLVIADCRFLSYMPSVLATATMLHVIHQVEPCNAADYQNQLLEVLNISKEKVNDC
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/protein_id="BAA76478.1"
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AJ250397.1 GI:6448481
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The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doonan, J.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1
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1 (bases 1 to 1140)
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                                                                                              /protein_id="Cab61222.1"
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/protein_id="Cab61222.1"
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FSALTAVLAVWYLDRFLCTFOFQODKFWMYOLAVGLSLAAKVEETOVFLLLLLCKEFLNRCEC
ESKYVFESKTIQRMELLVLSTLKWKMNPYTPISFLEYIARRLALKSHLCKEFLNRCEC
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                                                          KLIQEVATSVHFQSGNKRKFGSLPYSPKGVVDISFSCDDSWPLDSTASVSSSPEHLSF
                                                                               LLLSLITDCRFMCHLPSALATATMLYVISSLEPCIGVEYQDQLINILGINKDKVEECC
                                                                                                                                                                                                                                                                                  /gene="cycD3a"
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/db_xref="taxon:4151"
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for cyclin D3a
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Solanam;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
AJ002589
                                                    Submitted (11-NOV-1997) Kvarnheden A., Mt Albert The Horticulture and Food Research Institute of Private Bag 92169, Auckland, NEW ZEALAND
                                                                                                                                                                                                                                                                                                                                                                                           AJ002589.1 GI:6434198
2 gene; CycD3: D-ture
                                                                                                                                                                                     development in tomato
J. Exp. Bot. 51 (352), 1789-1797
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Isolation of three distinct CycD3
                                                                                                               Direct Submission
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                                                                                                                                                  (bases 1 to 1460)
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/organism="Lycopersicon
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for D-type cyclin.
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Sequence 5 from Patent
A85061
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/codon_start=1
/protein_id="CAB60837.1"
/db_xxef="GI:6434199"
/db_xxef="SPTREMBL:09SMD5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KISKENVNNCYELISEVSSKPITSHKRKYDENDSSPSGVIDPITTSESSNDSWDLDLP
SFKKSKVQEQQMKMSSSLSRVFVEAVGSPH"
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QVPLLLDFQVEDAKYVFEAKTIQRMELLVLSSLKWRMNPVTPLSFLDHIIRRLGLKNN
VHWEFLRRCESLLLSVMIDCRFVRYMPSVLATAIMLHVIHQIEPCNAIDYQNQLLGVL
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26. .1120
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GTTKTNSLLLLPLLLLEQDLFWEDEELLSLFVKEKETRCCFESFGSDPFLCSARVDVV
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/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                               GATTCAAGATTCGTGTTATAAACCATCCGTGTTGGCCACAGCTACAATGCTTCACGTT
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PLANTS WITH MODIFIED GROWTH

Patent: WO 9842851-A 5 01-OCT-1998;

MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE

Location/Qualifiers
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                                                         A.thaliana mRNA for cyclin delta-2
X83370
Arabidopsis thaliana
              CycD2; cyclin; cyclin thale cress.
                                            x83370.1 GI:2995131
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/db_xref="taxon:4233"
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                              D2; cyclin delta-2
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                                                                                                      335 GAGCGCAACTTCGTTCCGGGATTCGAGTACCTGTCGCGGTTCCCAATCTCGCTCCCTGGAC 394
474
                                     395
TTGTCTGTTCGAAACCAAGCTCTTGATTGGATTCTAAAGGTTTGTGCTCATTACCATTTT
                  GCCAACGCCAGAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTT
                                                                             GAGATTGAGTTTTGCCCCTGGAACTGATTATGTTAAGAGATTGCTTTCTGGTGATTTGGAT 473
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Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-JUN-1996)
Cambridge, Tennis Court
revised by [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK On Mar 28, 1998 this sequence version replaced g1:1402895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
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/note="pest motif, potential"

/note="pest motif, potential"

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/traisiation="maenlacgetseswiidndddinygggftneidlsvengald
wigkngsipwagssssslsedrikemlurelefcpgtdyvkrllsgdldlsvengald
wilkvcahyhfghlciclsmyldreilsyelpkdkmakdlalgscleaskmeetd
vphtydlovedpkfyveaktikrmellvyttlnwrloaltpfsfidveydkisghyse
nliyrssrfilnttkaiefldfrpseiaaaavsvsisgetecideekalssliyvko
erykrclnlmrsligeenvrgtslsoeqarvavravpaspvgvleatclsyrseertv
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/protein_id="CAA58286.1"
/db_xref="GI:2995132"
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/clone_lib="pfL61"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                   /note="cyclin box"
                                                                                                                                                                                                                                                                                                                                                                                                        /note="pest motif, potential"
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                                                                                                                                                              Mismatches
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                                                                                                                                                                                                    Submitted (20-JUN-1995) H. Hirt, Inst. of Microbiology & Univ. of Vienna, Dr. Bohrgasse 9, 1030 Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                              The D-type alfalfa cyclin gene cycMs4 cyclin-deficient yeast and is induced
                                                                                                                                                                                                                                                                                                                                                               Dahl, M., Meskiene, I., Bogre, L., Ha, D.T., Swoboda, Hirt, H. and Heberle-Bors, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclin; cycMs4 gene.
Medicago sativa.
Medicago sativa
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           /codon_start=1
/product="cyclin"
/protein_id="CAA61334.1"
/db_xref="GI:1150932"
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_xref="SPTREMBL:Q40338"
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                                                                                           CATTGGGAGTTTCTTAGGCGCTGTGAGAATCTTCTTCTATCTGTACTTTTAGATTCAAGA
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                                                                                                                                           ATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAGAGGCTAGC
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SSDGSNDSWTVGASSYSTSEPVFKKTKNQGQNMNLSPINRVIVGILATATSP"
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0; Mismatches 207;
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                                                         JOURNAL
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                                                                   Renz,A., Fountain,M. and Beck,E.
Nucleotide sequence of a cDNA encoding a
photoautotrophic cell suspension culture
                                                                                                                              Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 95447 Bayreuth, FRG 2 (bases 1 to 1699)
                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
                                                                                                                                                                                                                                                                                                                                 Chenopodium rubrum
                                                                                                                                                                                                                                                                                                                                                                      cycD1 gene; cyclin-D like protein
                                                                                                                                                                                                                Direct Submission
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                                    Location/Qualifiers
/organism-"Chenopodium
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                                                                                                            GACCTTCAGAAATAGCAGCAGCAGTGGCAATTTCTGTAACACAGCAAA 1192
                                                                                                                                                        GGCCTTCATGCATTGCTGCTGCAGCCATACTCACTGCAGCTAATGAAA 890
                                                                                                                                                                                                   TTTTTCAAGCCATCCAACTCATCCTAAGCACAATCAAAGGAATTGACTTGATGGAATTCA 1144
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SDDTSTTPSGSCGNSAHSSPASAPPPKRRKLDRTSQIS"
283 c 308 g 552 t 2 others
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lrnerddettlillik generalisgefvanheclaslednerhelgldylkrenng
Dldlgarnlyldmihkygshynegplcyvlsvnyldrelsayelpgkanmqdldyse
Lslaakydetdyptlildqyseskfyfeakiiqnaeliylstlkmrmqsytpeseidy
Elyklsgdkneskslifqaiqlillstingidlmefreseidaavalsytqqqqiveft
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/protein_id="CAA71244.1"
/db_xref="GI:1770190"
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385. .1503
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/clone="pBluescript II SK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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DLLWEEEELTSLFSKETEYEISYNVLEKNQSFISSRRESVEWILKTTAYYSFSAQTGF
LAVNYFDRFILFSFNQSLNHKPWMNQLYAVTCLSLAAKVEETDYPLLLDLQVEESGFL
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101. .1111
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/cultivar="UC82B"
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A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK On Mar 28, 1998 this sequence version replaced g1 603508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray, J.A.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Bhotechn., Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                 SSSPFVVLQQDLFWEDEDLVTLFSKEEEQGLSCLDDVYLSTDRKEAVGWILRVNAHYG
FSTLAAVLAITYLDKFICSYSLQRDKPWMLQLVSVACLSLAAKVEETQVPLLLDFQVE
ETKYVFEAKTIQRWELLILSTLEWKMHLITPISFVDHIIRFLGLKNNAHWDFLNKCHR
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/protein_id="RAS8287.1"
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/db_xref="G1:2995134"
/db_xref="SWISS-PROT:P42753"
/translation="MAIRKEEESREEQSNSFLLDALYCEEEKWDDEGEEVEENSSLSS
                                                                                                                                                                                                      /dev_stage="seedling, stage 2 leaves"
266. .1396
                                                                                                                                                                                                                                                                                      /variety="ecotype Land"
LLLSVISDSRFVGYLPSVVAAATMMRIIEQVDPFDPLSYQT|NLLGVLNLTKEKVKTCY
                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                               /tissue_type="whole seedlings"
/clone_lib="pFL61"
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                   GCGAGGGACTAAGAAAAAGAAAAAGTAATAGGGTGCTACCAGTTGATGCAAGAGCT 990
                                                              GAATTATAGAGCAAGTTGATCCCTTTGACCCTCTTTCATACCAAACTAATCTCCTCGGTG
                                                                                                                                                                                                                              CAACTGGAACTTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATA 815
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                                                                                               CTGCAGCTAATGAAATTCCTAATTGGTCTGTGGTTAAGCCCCGAAAATGCTGAGTCATGGT 935
                                                                                                                                                                                               TTAAGAACAATGCTCACTGGGATTTCCTCAACAAATGCCACCGTCTCCTCCTCTCTGTAA 935
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                                                                                                                                                            TCCAAGAGGCTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTCA 875
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1169. .1393
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CNPPTSSSSPQQQPPLKKMRGAEENEKKKPILHLPWAIVATP"
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Copyright (c) 1993 - 2002 Compugen
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Soybean cyclin del
Soybean cyclin del
Arabidopsis thalia
H.tuberosus CYCD1;
N. tabacum CYCD3;1
H.tuberosus CYCD3;1
H.tuberosus CYCD3;2
Arabidopsis thalia
N. tabacum CYCD3;2
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## ALIGNMENTS

RESULT 1 AAZ19958

AAZ19958 standard; cDNA; 2259

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WPI; 1999-591036/50
         Cahoon
                           23-MAR-1998;
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         Orozco
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Cyclin delta-1; soybean; cell cycle; cell division; transgenic plant; herbicide; plant breeding; ss.

Soybean cyclin delta-1 cDNA

21-DEC-1999 AAZ19958;

(first entry)

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WPI; 1999-591036/50.
P-PSDB; AAZ31895.
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New isolated plant cyclin genes, used to develop products for use herbicides and for developing plant breeding programs -25

Claim 7; Page 53-54; 68pp; English

chine se6, pk0028.fll encoding a portion of the cDNA insert in colone se6, pk0028.fll encoding a portion (see AA731895) of a soybean cyclin delta-1 protein. The clone was isolated from a soybean cc embryo (26 days after flowering) cDNA library. The invention cc embryo (26 days after flowering) cDNA library. The invention cc encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 cc encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 cc encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin, in sense cc of chimeric genes encoding all or a portion of a cyclin, in sense cc or antisense orientation, where expression of the chimeric gene cc or antisense orientation, where expression of the chimeric gene cc results in altered levels of the cyclin protein in a transformed chost cell. This would have the effect of altering the regulation of of cell division in those cells. The nucleic acid fragments may be cused to express cyclins in plant cells to enhance cell tissue culture growth. The availability of nucleic acid sequences encoding call or a portion of cyclins should facilitate studies of cell cycle collure, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets cc collurae, increase the efficiency of gene transfer and help provide coll collure, increase the efficiency of gene transfer and help provide collures table transformations. The proteins can be used as targets cc enzymes that may be useful as herbicides.

1994 BP; 534 A; 361 C; 477 G; 622 T; 0 other;

멍 δÃ 당 δÃ Qy 밁 δÃ δō 밁 δÃ В δÃ 밁 Ş 맑 Q Š 밁 밁 Best Local Matches 136 Query Match 824 472 412 584 292 172 407 112 347 52 GCTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTCACTGCAGCT TCCTCGCCGCCGTCGGAGGCGGAGTCCATCGCCGGATTCATGGAAGACGAGCGCAACTTC GAGCCGAGAACAATTCGTAGGATGGAGCTACTTGTTCTCGGTGTCTTAGATTGGAGGCTA ACAAATGGGTGGCCTCTGCAACTTGTATCTGTTGCATGCTTTGTCTTTTGGCAGCAAAGATG GCGTACCTCGCCGTCAACTATATGGATCGGTTTTTTGGATTCTCGCCGGTT----GCCGGAA GTTCCGGGATTCGAGTACCTGTCGCGGGTTCCAATCTCGCTCCCTGGACGCCAACGCCAGA TCGCCGACGACAGAGGATTGTTATTCGATCGCGAGCTTCATCGAGCACGAGCGCAACTTC al Similarity 1363; Conserv ACTTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAGAG GAAGAACCTCTTGTTCCATCTCTCTGGACCTTCAGATAGAAGGTGCCAAGTACATATTT GAAGAATCCGTTGCATGGATTCTCAAGGTGCAGGCTTATTACGCTTTTCAACCGGTCACG GAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTCAGCCTTTGACG GTCCCCGGATTCGAATACCTCAATAGGTTCCAATCTCGCTCTCTCGACGCCTCTGCCAGA ACTTTTACCGGGTTCCTCATTTCACGTGCTACACAAATTATCTTATCTAATATACAAGAG ACGAATGGGTGGCCACTGCAACTTCTCTCTGTTGCGTGCTTGTCTTTAGCAGCAAAGATG GCTTATCTTTCCGTTAACTACTTGGATAGGTTCTTGAATTCTCGACCGTTGCCGCCGAAA Conservative 30.5%; Pred. No. le0; Mismatches Score 689.6; Pred. No. le le-163; DB 20; Length 519; Indels 152; Gaps 531 763 471 703 411 643 583 291 523 231 466 171 406 111 351 21;

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                                                                                                                                                                                                                                                                                                                                                                                       TAAAAAGAATGGAACTTCTTGTTCTAAGTGTGTTAGATTGGAGACTAAGATCGGTTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTTAACTATATGGATCGGTTTCTTTACGCTCGTCGATTACCGGAAACGAGTGGTTGGC
                             TGAGGTCAAGTACTGTATCATCATCTCATCCTCTTC
                                                                                GGAAACTCCCCTTACTAAAAGTGTTGCCGCAGCTGCGAGTAA----CAACTCGGACCCGAA
                                                                                                                                       AAGAMAAAGTAATAGGGTGCTACCAGTTGATGCAAGAGCTTGTGATTAACAATAACCAAC
                                                                                                                                                                                                                                                  CTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTCACTGCAGCTAATGAAATTCCTA
                                                                                                                                                                                                                                                                            TAAATACACCAAAAGTGATAGCAAAGCTTCGAGTGAGTGTAAGGGCATCATCGACGTTAA
                                                                                                             AAGAGAAGATAGTGAGATGCTATAGACTGATGAAAGCGATGGCCATCGAGAATAACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161405.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161361.
99US-0161992.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                             -TGTGGTTAAGCCCGAAAATGCTGAGTCATGGTGCGAGGGACTAAGAA
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68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 388.4;
Pred. No. 8.4e
0; Mismatches
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                             1107
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CDC; Rb; retinoblastoma;
root development; ds.
                                                                                                                                                                                                                                                                                                                                     This sequence represents the CYCD1;1 CDNA from Helianthus tuberosus which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helianthus tuberosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulating growth and structure of plants by modulating protein controls cell division - specifically a D-type cyclin, and relat chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; p56-57; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-532012/45.
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                                                                                                                                                                                                                                                                                               Sequence 1788 BP;
                                                                                                                                                                                                                                                                                                                            carnation,
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                                                                                                                     344
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                                                            404
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                                                                                                                                   TTATTCGATCGCGAGCTTCATCGAGCACGAGCGCAACTTCGTTCCGGGGATTCGAGTACCT
                                                                                                                     CGAGCGATTTCAATCGCAAGTTCTCGATGCTTCTGCTAGAGAAGAATCGGTTGCCTGGAT
                TATGGATCGGTTTTTGGATTCTCGCCGGTTGCCGGAAACAATGGGTGGCCTCTGCAACT
                                                            CCTTAAGGTGCAACGGTTTTACGGATTTCAGCCGTTGACGGCGTACCTCTCCGTTAACTA
                                                                            TCTCAAGGTACACGCGTACTATGGCTTTTCAGCCTTTGACGGCGTACCTCGCCGTCAACTA
   TCTGGATCGTTTCATCTATTGCCGTGGCTTCCCGGTGGCAAATGGGTGGCCCTTGCAACT
                                                                                                                                                                                                                                        492;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                            chrysanthemum, rose, tulip, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYCD1;1
                                                                                                                                                                                                                                      16.8%;
ilarity 72.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMBRIDGE TECH SERVICES
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                                                                                                                                                                                                                                                                                                 511 A; 386 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; cell-division control; phosphorylation;
a; germination; flowering; seed; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                      Score 379.8;
Pred. No. 1.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                 387 G; 504 T; 0 other;
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                                                                                                                                                                                                                                         187;
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Gaps

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RRESULT 5
AAV33885
ID AAV3
XX AAV3
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AC AAV3
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CCC;
KW CCC;
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XX N1co
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XX PN W098
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This sequence represents the CYCD3;1 cDNA from Nicotianal tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-type cyclin; growth; plant; cell-division control; p CDC; Rb; retinoblastoma; germination; flowering; seed;
                                                                                                                                                                       Regulating growth and structure of plants by modulating controls cell division - specifically a D-type cyclin, a chimeric genes and transformed cells and plants, used to growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. tabacum CYCD3;1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV33885 standard;
                                                                                                                                       Claim 14; p54; 75pp; English.
                                                                                                                                                                                                                                                              WPI; 1998-532012/45.
                                                                                                                                                                                                                                                                                                Murray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     root development; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATGCATTGCTGCTGCAGCCATACTCACTGCAGCTAATGAAATTCCTAATTGGTCTGT
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d; fruit;
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TTGAACTCATATCAGAAGTGTGTTCTAAGCCCATTTCACACAAACGC
                                                                                                                                                                                                                                                     ATCATATTATAAGGAGGCTTGGGCTAAGAAATAATATTCACTGGGAATTTCTTAGAAGAT
                                                                                                                                                                                                                                                                                  CTTTCTTTGCGTGCAAAGTAGATTCAACTGGAACTTTTATCCGGTTCCTTATTTCCAGGG
                                                                                                                                                                                                                                                                                                                 TTTTAGTGTTGTCTTCACTAAAATGGAGGATGAATCCAGTGACCCCACTTTCATTTCTTG
                                                                                                                                                                                                                                                                                                                                      TACTTGTTCTCGGTGTCTTAGATTGGAGGCTAAGATCAGTAACACCACTTTGCTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                            ATTTTCAAGTGGAGGATGCTAAATATGTGTTTGAGGCAAAAACTATTCAAAGAATGGAGC
                                                                                                                                                                                                                                                                                                                                                                                              ACCTTCAGATAGAAGGTGCCAAGTACATATTTGAGCCGAGAACAATTCGTAGGATGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTACTTGTCTTTAGCTGCTAAAGTTGAAGAAACTCAAGTTCCTCTTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGTTTCTGACTAGTCTTCATTATCAGAAAGATAAACCTTGGATGATTCAACTTGCTG
                             ACCAGTTGATGCAAGAGCTTGTGATTAACAATAACCAACGGAAACTC 1018
                                                                                         AGCCCGAAAATGCTGAGTCATGGTGCGAGGGACTAAGAAAAAGAAAAAGTAATAGGGTGCT
                                                                                                                       TATTGGCCACTGCAATTATGCTTCACGTTATTCATCAAGTTGAGCCTTGTAATTCTGTTG
                                                                                                                                                                                       GTGAAAATCTCCTCCTCTATTATGGCTGATTGTAGATTCGTACGTTATATGCCGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 281 C; 293 G; 568 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rose, tulip, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152.6; DB pred. No. 3e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309; Indels
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AAV33888 standard; cDNA to mRNA; 1414 ΒP

AAV33888;

25-JAN-1999 (first entry;

H.tuberosus CYCD3;1 gene

RESULT 6
AAV33888
IID AAV3
XX AAV3
XX AAV3
XX AAV3
XX LAV3
DT 25-J
XX D-ty
KW CDC;
KW CDC;
KW roott
XX FOOT
XX Heli
XX Heli D-type cyclin; CDC; Rb; retin development; retinoblastoma; growth; plant; ds. germination; cell-division control; phosphorylation; ination; flowering; seed; fruit;

Helianthus tuberosus

W09842851-A1

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Best Local S
Matches 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the CYCD3;1 cDNA from Helianthus tuberosus which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulating growth and structure of plants by modulating protein controls cell division - specifically a D-type cyclin, and relationship genes and transformed cells and plants, used to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; p58; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1414 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carnation, chrysanthemum, rose, tulip, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
                                                                                                                                                                                               621
                                                                                                                                                                                                                                                                                               641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGACGGCGTACCTCGCCGTCAACTATATGGATCGGTTTTTTGGATTCTCGCCGGTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTCAGCCT 460
                                                                                                                                                                                                                                                                                  TTTGAGCCGAGAACAATTCGTAGGATGGAGCTACTTGTTCTCGGTGTCTTAGATTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                               GAAGATAAACCTTGGATGATTCAACTTGTTGCTGTTAGTTGTCTCTCTTTAGCTGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCGTAAAGAGGCTGTAGATTGGATCCTTAAGGTCAAAAGTTGTTATGGATTCACACCT
                            GCTAATGAAATTCCTAATTGGTCTGTGGTTAAGCCCCGAAAATGCTGAGTCATGGTGCGAG
                                                                                                                               GATCATGTTCATTGGGATTTTTTCAAGAAATGTGAAGCTATGATCCTTTGTTTAGTTTCA
                                                                                                                                                  GGAACTTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAA
                                                                                                                                                                                                                              CTAAGATCAGTAACACCACTTTGCTTCCTCGCTTTCTTTGCGTGCAAAGTAGATTCAACT
                                                                                                                                                                                                                                                              TTTGAGGCTAAAAACATACAAAAAATGGAGCTTTTGGTGATGTCAACTTTGAAATGGAGG
                                                                                                                                                                                                                                                                                                                               GTTGAAGAAACTCAAGTGCCACTCTTACTAGATCTTCAAGTAGAGGACACTAAGTACTTG
                                                                                                                                                                                                                                                                                                                                                             ATGGAAGAACCTCTTGTTCCATCTCTCTGGACCTTCAGATAGAAGGTGCCAAGTACATA
GTAGATGAAATTGATCCTCCCAATTGTATTGACTACAAAAGTCAACTTCTGGATCTTCTC
                                                              GATTCAAGATTCGTGTTATAAACCATCCGTGTTGGCCACAGCTACAATGCTTCACGTT
                                                                                              GAGGCTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTCACTGCA
                                                                                                                                                                                              ATGAACCCAGTGACACCAATCTCATTTCTTGATCACATTGTAAGAAGGCTTGGATTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rate, flowering, seed production etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 A; 276 C; 248 G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%;
51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 134.4;
Pred. No. 1.1
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RESULT 7
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                                                                  24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
                                                                                                                                                                                                                                     23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                               16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
                                                                                                                      19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
                                                                                                                                                                         14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolic pathway; promoter; termination sequence; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation assay; genetic mapping; gene expressio protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC40202 standard; DNA; 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment
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07-MAY-1999;
                                                                                                                                                                                                                     05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                   08-APR-1999;
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23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000;
                                                                                                                                                                   14-MAY-1999;
                                                                                                                                                                                            11-MAY-1999;
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                                                                                                                                                  18-MAY-1999;
                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACTAAGAAAAAAAAAAGTAATAGGGTGCTACCAGTTGATGCAAGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACCACTAAGGACGACATAAACGAGTGTTACGAGCTCATTGTCGAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                        2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
 990S-0137724.
990S-0138094.
990S-0138540.
990S-0138847.
990S-0139119.
990S-0139452.
990S-0139453.
                                                           99US-0130510
99US-0131449
99US-0132048
99US-0132484
99US-0132485
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99US-0130449.
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                                                                Query Match
Best Local Similarity 50.3
Matches 302; Conservative
                                                                                                      13-AUG-1999
16-AUG-1999
17-AUG-1999
18-AUG-1999
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           464
                              451
                                                404
ACGGCGTACCTCGCCGTCAACTATATGGATCGGTTTTTGGATTCTCGCCGGTTGCCGGAA
                           AGGAAAGAGGCTTTAGATTGGGTTCTTAGGGTTAAATCTCATTATGGGTTTACTTCATTG
                                        AGAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTCAGCCTTTG
                                                                                                       99US-0148684

99US-0149175

99US-0149175

99US-01491723

99US-0149929

99US-0150864

99US-0150866

99US-0151065

99US-0151065

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99US-01513303

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99US-01513363

99US-01554038

99US-01554386

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99US-0159331

99US-0159331

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99US-0159331

99US-0159331

99US-0160741

99US-016081

99US-0161360

99US-0161360

99US-0161361

99US-0161361
                                                                          50.2%;
                                                                Score 122; DB 21;
Pred. No. 1.4e-20;
0; Mismatches 300;
                                                                                     Length 1311;
                                                                  Indels
                                                                 0:
                                                                 Gaps
          523
                           510
                                               463
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17-JUN-1999
18-JUN-1999
18-JUN

9905-0139452
9908-0139453
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9908-0139461
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RESULT 8
AAV33886
ID AAV3
XX
AC AAV3
XX
DT 25-J
XX
CDC;
XW CDC;
XX Nico
OS Nic
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                       Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-type cyclin; growth; plant; cell-division control; phosphorylation;
CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N. tabacum CYCD3;2 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the CYCD3;2 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, malze, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1431 BP; 387 A; 267 C;
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                             N. tabacum
                                                                                                                       AAV33884 standard;
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                                                                                                                                                                                                   TTAAAGTCAAACAGGATAGTTTTGAAGAATGCCATGATCTTATTCTAGAGCTAATG 1058
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                            CYCD2;1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the CYCD2:1 cDNA from Nicotian tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase coot development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulating growth and structure of plants by modulating protein that controls cell division - specifically a p-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; p52-53; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1284 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carnation, chrysanthemum,
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762
                                                                                              705
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                                                                                                                                                                                                                                                                                                                                                       TGAGAAAAGAGGCTCTTGATTGGATTTTGAAGGCTCATATGCACTATGGATTTGGAGAGC
                                                                                                                                                                                                                                             AAACAAATGGGTGGCCTCTGCAACTTGTATCTGTTGCATGCTTGTCTTTGGCAGCAAAGA 581
                                                                                                                                                                                                                                                                                                                                                                                     CCAGAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTCAGCCTT
GAACTTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAG
                                                              TAAGATCAGTAACACCACTTTGCTTCCTCGCTTTCTTTGCGTGCAAAGTAGATTCAACTG
                                                                                                              TTGAGCCGAGAACAATTCGTAGGATGGAGCTACTTGTTCTCGGTGTCTTAGATTGGAGGC
                                                                                                                                                            TGGAAGAAATTAATGTTCCTTTGACTGTTGATTTACAGGTAGGGGATCCCCAAATTTGTAT
                                                                                                                                                                                          TGGAAGAACCTCTTGTTCCATCTCTCTTGGACCTTCAGATAGAAGGTGCCCAAGTACATAT
                                                                                                                                                                                                                          GAAGTAAAACTTGGACAGTGCAATTGTTAGCTGTGGCCTGTCTATCACTTGCAGCCAAAA
                                                                                                                                                                                                                                                                                          TGAGTTTTTGTTGTCGATAAATTACTTGGATCGATTTCTATCTCTGTATGAAATTGCCAA
                                                                                                                                                                                                                                                                                                             TGACGGCGTACCTCGCCGTCAACTATATGGATCTGTTTTTTGGATTCTCGC¢GGTTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTTTTGCCTAAAGATGATTATGTCGAGAGATTGAGAAGTGGAAGATTTGGATTTGAGTG
                                                                                              TTGAAGGCAAAACTATACAAAGAATGGAACTTTTGGTATTAAGCACATTGAAGTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMBRIDGE TECH SERVICES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0302096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 A; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      germination; flowering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 116.8;
Pred. No. 2.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tulip,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8e-19;
ches 272;
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CC gene that encodes cyclin D (CycD, see AA79323), a protein necessary CC for progression from G1 into S phase. The encoded protein binds to CDX4, and the active CycD-CDX4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which CC activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AA79321-24) CC that are involved in cell cycle regulation. Also provided are creombinant expression cassettes (including ZmCycD in sense or creombinant expression cassettes (including ZmCycD in sense or consistence orientation), host cells, transgenic plants (especially CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or collseed Brassica) and antibody compositions. A claimed method of CC modulating the level of CycD protein in a cell comprises CC transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and CC growing the cell for a time sufficient to induce expression of the CC plynucleotide sufficient to modulate (increase or decrease) the CC grop protein in the cell. The CycD protein is present in an amount CC sufficient to alter cell division, increase the number of cells concrease the growth rate, increase crop yield, alter plant cheight or size, enhance or inhibit organ (seed, root, shoot, ear, CC tassel, stalk, pollen, stammen) growth, produce organ ablation, cCC produce parthenocarpic fruits, produce male sterile plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize cyclin D ZmCycD gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 122-124; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoerster GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowe KS,
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DB; AAY79323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1173 BP; 200 A; 366 C; 416 G; 191 T; 0 other;
                                                   06-SEP-2000
                                                                                    EP1033405-A2
                                                                                                                    Arabidopsis thaliana
                                                                                                                                                      metabolic
                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 68616.
                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                        AAC51463;
                                                                                                                                                                                                                                                                                                                       AAC51463 standard; DNA; 1356
                   25-FEB-2000; 2000EP-0301439
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                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCCTGAACAA 617
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTTGCGTGCAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTTCTCGGTGTCTTAGATTGGAGGCTAAGATCAGTAACACCACTTTGCTTCCTCGCTT
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                                                                                                                                                    pathway; promoter; termination sequence; ss.
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Pred. No. 3.9
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     25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999
   23-JUN-1999;
24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
01-JUL-1999;
01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
08-JUL-1999;
09-JUL-1999;
12-JUL-1999;
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17-JUN-1999;
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24-MAY-1999;
25-MAY-1999;
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05-MAY-1999;
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10-JUN-1999;
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28-MAY-1999;
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Best Local Similarity 52...
Matches 254; Conservative
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                                            CTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTGCAGCTA
                                                                                                                                                                        ATCATCAATTGGAGTTCTTGAGTAGATGTGAATCTTTATTACTCTCCATTATTCCTGATT
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                                                                                        CTTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAGAGG
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Pred. No. 4.6e-19;
0; Mismatches 230;
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31-AUG-1999;
01-SEP-1999;
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                                                                       GAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTTGAGCCTTTGA 464
CAAATGGGTGGCCTCTGCAACTTGTATCTGTTGCATGCTTGTCTTTGGCAGCAAAGATGG
                    CGGCTCTTTTAGCTGTTAATTACTTCGATAGGTTTATTACAAGCAGGAAGTTTCAGACAG
                                         CGGCGTACCTCGCCGTCAACTATATGGATCGGTTTTTTGGATTCTCGCCGGTTGCCGGAAA 524
                                                            GTGAAAAGGCTCTTGATTGGATTTTTAAAGTGAAATCTCATTATGGGTTTAATTCATTGA
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                                                                                                             Score 116; DB 21;
Pred. No. 4.6e-19;
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                                                                         CTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTCACTGCAGCTA
                                                                                                  ATCATCAATTGGAGTTCTTGAGTAGATGTGAATCTTTATTACTCTCCATTATTCCTGATT
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                                                  CGAGATTTCTGAGTTTTAGTCCTTCTGTGTTAGCCACTGCAATAATGGTCTCTGTTATTA
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AAV33889 standard; cDNA to mRNA; 1846 ₽P

AAV33889;

25-JAN-1999 (first

entry)

Maize CYCD2 gene

D-type cyclin; growth; pi CDC; Rb; retinoblastoma; development; plant; cell-division control; phosphorylation;
a; germination; flowering; seed; fruit;

mays.

W09842851-A1

01-OCT-1998

24-MAR-1998; 98WO-EP01701

26-MAR-1997; 97EP-0302096.

Murray

(UYCA-) UNIV

CAMBRIDGE TECH SERVICES LTD.

1998-532012/45.

Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.

Claim 14; p64-65; 75pp; English.

ARESULT 13
AAV33889
JID AAV33889
JID AAV33889
AC AAV33
AC AAV34
AC AAV4
AC AA This sequence represents the CYCD1;1 cDNA from Zea mays which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase number of flowers, seeds or fruits per plant, increase root development,

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1846 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carnation, chrysanthemum, rose, tulip, etc.
                                                                                                                                                                                                                  Maize; cyclin D;
                                                                                                                                                                                                                                            Maize cyclin D ZmCycD gene
                                                                                                                                                                                                                                                                         18-JUL-2000
                                                                                                                                                                                                                                                                                                   AAZ94581;
                                                                                                                                                                                                                                                                                                                              AAZ94581 standard; DNA; 1861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455
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 23-SEP-1998;
                            21-SEP-1999;
                                                       30-MAR-2000
                                                                                    WO200017364-A2
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 98US-0101551
                            99WO-US21946
                                                                                                                              Location/Qualifiers 275..1351
                                                                                                                                                                                                                  ZmCycD gene;
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                                                                                                                                                                                                                  CycD; cell division; cell cycle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233; Indels
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WPI; 2000-283589/24
P-PSDB; AAY79321.
                                                                                                 (PION-) PIONEER HI-BRED INT INC.
                                                                                           . GJ:
                                                                                             Tao Y,
                                                                                              Gordon-Kamm WJ,
                                                                                              Gregory CA,
                                                                                              McElver
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Novel polynucleotides related proteins and a s encoding maize cyclin D antisense RNA useful for control of cell cy nd 3, cycle

Claim 1; Page 115-117; 134pp; English

cc modulating the level of CycD protein in a cell comprises
CC transforming the cell with a recombinant expression cassette
CC comprising a CycD polynuclectide linked to a promoter, and
CC growing the cell for a time sufficient to induce expression of the
CC growing the cell for a time sufficient to induce expression of the
CC cycD protein in the cell. The CycD protein is present in an amount
CC sufficient to alter cell division, increase or decrease) the
CC dividing, improve transformation frequencies, alter cell growth,
CC increase the growth rate, increase crop yield, alter plant
CC tassel, stalk, pollen, stamen) growth, produce organ ablation,
CC produce parthenocarpic fruits, produce male sterile plants,
CC enhance embryogenic response, increase callus induction, provide
CC cycle, improve response to environmental stress including
CC protein in the cells is transiently modulated by introducing
CC cycl RNA or Cycl polypeptides. Cycl polynucleotides can be used
CC cycl RNA or Cycl interacting proteins. All claimed. gene that encodes cyclin D (CycD, see AN7/9321), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AN294581-84) and polypeptides (see AN79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alifalfa or oilseed Brassica) and antibody compositions. The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (CycD, see AAY79321), a protein nec A claimed method of

Sequence 1861 BP; 462 A; 413 C; 512 G; 474 T; 0 other;

Best Loc Matches Query Match Local 252; Similarity Conservative 5.0%; 52.0%; 0; Score 112.2; Pred. No. 4. Mismatches .9e-18; DB 21; 233; Indels Length 0; Gaps

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δã 밁 QΥ 망 Ş Ş 밁 455 569 395 GCCAACGCCAGAGAAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTT 454 575 GCAAAGATGGAAGAACCTCTTGTTCCATCTCTCTGGACCTTCAGATAGAAGGTGCCAAG 629 GCACCGTTGACTGCCGTTTTGTCTGTGAACTACCTCGATAGATTCCTCTCCACGTATGAG CAGCCTTTGACGGCGTACCTCGCCGTCAACTATATGGATCGGTTTTTTGGATTCTCGCCGG GCCGCCGTCAGGAAGGACGCCATCGATTGGATTTGGAAGGTCATTGAGCATTACAATTTC TIGCCGGAAACAAIGGGIGGCCICIGCAACIIGIATCIGIIGCAIGCIIGICTIIGGCA 574 514 628 748 688

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                                                                                                                                                                                                                                    related proteins and regulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200017364-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize; cyclin D; ZmCycD gene; CycD; cell division; cell
                                                                                                                                                                                                            Claim 1; Page 120-121; 134pp; English.
                                                                                                                                                                                                                                                   Novel polynucleotides encoding maize cyclin D isoforms related proteins and antisense RNA useful for control c
                                                                                                                                                                                                                                                                                          P-PSDB; AAY79322
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comprising a CycD
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 linked to a promoter,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1077 BP; 228 A; 265 C; 308 G; 276 T; 0 other;
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                                                                                                     ATCCAAGAGGCTAGCTTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATACTC 874
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Similarity 51.8%;
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                                                                                                                                      Description
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2 sab63e07.
2 sab62f07.
2 se3T508741
1 eST512732
2 eST535463
1 eST457690
1.1 eST45740
2 eST495740
8 ss68e07.y
L eST335726
                                                                                                                                                                                  REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
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BI427409
                                                                                                                        COMMENT
                                       FEATURES
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                                                                                                                              TITLE
JOURNAL
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105.4	105.4	105.4	105.4	107	108.8	109	112.2	113.2	113.6	118	125	126.6	126.6	127.2	129.2	129.4	132.8	134.4	141	142	145.6	149	166	69	9	205.6	11	
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727	727	725	546	516	478	608	558	790	485	621	666	802	731	523	659	596	478	546	813	583	557	197	287	515	585	501	658	
5	10	10	10	10	9	9	9	10	10	10	10	10	10	10	10				10		10	10	10	10	10	10	ø	
ĕ	7	BI203937	39	ĭ			AW036252	в1306295	0	BE442681	Ξ	BI207010	BM408328	BE472243	50	AW042725	BE472260	AW944884	BE642779	AI812774	933	591	E8014	32369	59506	3633	18	
EST52313	EST52275		EST52293	EST52908	W5279	EST33664	EST27833	NL_4_B	EST46	WHE110	EST528	EST52505	EST58265	EST41709	GAEa00	ST24F07	EST417		r12_6	AI812774 18H7 Pine	ak57d1	F073G	r14e07.	F005D03	ST4937	332 EST53909	T39238	

## ALIGNMENTS

DEFINITION

BI427409

BI427409

DEFINITION

ID: Gm-c1049-4594 5', mRNA sequence.

ACCESSION

REYNORDS

EST

SOURCE

ORGANISM

Glycine max

EURATYOUTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Source

Clycine

Glycine

Glycine

AUTHORS

AUTHORS

AUTHORS

AUTHORS

R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

FITLE

JOURNAL

Unpublished (199)

COMMENT

Washington University School of Medicine

4444 Forest Park barkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

First High quality sequence stop: 421.

LOCATION/QUALITIEES

SOURCE

JOURNAL

J

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1424 TGCAGAATTCACCTAGGGAAGAGGGATTTTGCGACATGTTACCGTGGGAGAGGAAATGAG 1483
                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAGAATTCACCTAGGGAAGAGGGATTTTGCGACATGTTACCGTGGGAGAGGAAATGAG
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                                                                                                                                                                                                                   CTTTTTCTT 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCTGTGAGTGTGGAAGAAGAAGTGAGTTGCGGGCTGGAATTCAAAGTTTGCATTAAT
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                                                                                                                                                                                                                                                        TATTGGCACGTGTGCAGTCGGTTCTGGTGCGTGCCAATGAAGTGTGTACGTGTGATTTTT 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGTTCAATGTTCATATCATGGTATTCATAAGTCAAGCAAAGCTTCATTTCTTGGCCA 359
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                                                                                                                                                                             CTTTTTCTT 548
                                  B1785106
sai37all.yl Gm-c1065 Glycine
ID: Gm-c1065-5397 5' similar
DELTA-1. ;, mRNA sequence.
BI785106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DBIOB"
/lab_host="DBIOB"
/note="Yector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector. The ligated cDNA fragments were transformed into pH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

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                                  bp mRNA linear EST 30-NOV-2001 max cDNA clone GENOME SYSTEMS CLONE to SW:CGD1_ARATH P42751 CYCLIN
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1544

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240

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1784

300

LOCUS DEFINITION RESULT 2 B1785106

ACCESSION

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1964

540

1904

420

480

1844

360

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61

1484

BASE COUNT ORIGIN

Matches

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               GGCGAGGACTCCTCCGGAATCCTCTCCGGAGAGTCGCCGGAGTGCTCCTTCTCCGACATC
                                                                                                                                                CCGCTGCCGCCGCCCTCCTCATGTCGGTTTCCTGCCTCTCCGACTACGACCTCCTCTGC
                                                                                                                                                                                                     ----ACCGCCGGGGCTCCTCATGTCGGTTTCCTGCCTCTCCGACTACGACCTCCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae;
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Glycine max
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="germinating shoots"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-5397"
/clone_lib="Gm-c1065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker."
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96.3%;
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, Schurk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTTGGCAGCAAAGATGGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCGCCGGTTGCCGGAAACAATGGGTGGCCTCTGCAACTTGTATCTGTTGCATGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG585146 809 bp mRNA linear EST 11-EST486909 MHAM Medicago truncatula/clomus versiforme mixed library cDNA clone pMHAM-22A23 5' end, mRNA sequence.
BG585146
BG585146.1 GI:13600210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula/Glomus versiforme
Medicago truncatula/Glomus versiforme
Eukaryota; mixed EST libraries.
1 (bases 1 to 809)
                                                                                                                                                                                                                                                     Email: mjharrison@noble.org
Noble EST name: N380619e TIGR sequence name: MTDChl2TK
Information is available at: http://www.medicago.org
Seq primer: Sknod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                   Glomus versiforme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                           Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                               and Fraser,C.M.
ESTs from roots of Medicago truncatula after colonization
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrison, M.J., Liu, J., Town, C.D., Van
                                                                                                                                                                                                                                                                                                                                                  Samuel Roberts Noble Foundation 
0 Sam Noble Parkway, Ardmore, OK
                                                                                                                                                                                                                                                                                                                        Sam Noble Parkway, Ardmore, 580-223-5810 580-221-7380
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 27, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK:, Site_1: EcoRi; Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                              /cultivar="Medicago trui
/db_xref="taxon:119092"
/clone="pMHAM-22A23"
/clone_lib="MHAM"
                                                                                                                                                                                                                              organism="Medicago truncatula/Glomus versiforme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library
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ESTs from roots of Medicago
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Noble EST name: N381409e TIGR sequence name: MTDCK70TK More
information is available at: http://www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
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Samuel Roberts Noble Foundation
Samuel Roberts Noble Foundation
On Table Parkway, Ardmore, OK 73401
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/lab_host="E. coli strain XLOLR"
/note="Yector: pBluescript SK; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-incompation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinent labels and services of the company of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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Pred. No. 9.9e-70;
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BG646052
BG646052.1 GI
                                                                                                                                                                                                                                                              Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258,
Tel: 409 845 7707
Fax: 409 845 2891
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C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobii
Inoculation, 2001
Unpublished (2001)
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                                                                                                                                                                 available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                kate@mail.bio.tamu.edu
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with
meliloti"
                                                  /organism="Medicago truncatula"
/culitya="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-48G20"
/clone_lib="KV3"
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TCCGACTGCGAGCTCCTCTGCGGGGAGGACCTCGTCGGAGGTCCTCACCGGAGATTTACC
                                                                                                       GGGATTCGAGTACCTGTCGCGGTTCCAATCTCGCTCGCTGGACGCCAACGCCAGAGAAGA 411
                                                                                    TGGTTTCGACTACGTCTCAAGATTCCAATCTCGCTCTCTCGAATCCAGCACCAGAGAAGA
                                                                                                                                                                  TGCCGAGGAAGAGGAGTCGATTGCTGTTTTCATCGAGCACGAGTTCAAGTTTGTTCC
                                                                                                                                                                                   -----GAGGATTGTTATTCGATCGCGAGCTTCATCGAGCACGAGCGCAACTTCGTTCC
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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College Station, TX
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Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available at: www.medicago.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: kate@mail.bio.tamu.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XNOI; CDNA was prepared from polyA+ enriched RNA. The cDNI was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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Tel:
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NF004A12FL1F1097 Developing f
NF004A12FL 5', mRNA sequence.
                                                                                                                                                                                                                                       Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
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                                                                                                                                                                                                                                                                                                                                  Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.,Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              Medicago.
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                                                                                                                                                                                                         Sam Noble Parkway,
580 221 7391
580 221 7380
                                                                                                                                                                                           gdmay@noble.org
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture very young, developing, fully-opened flowers and flower
                                               /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF004A12FL"
/clone_lib="Developing flower"
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BG238202 480 sab63e07.y1 Gm-c1043 Glycine ID: Gm-c1043-4046 5' similar
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/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
eNAN from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-ZAP XR vector
using ExAssist helper phage and the E. coli strain
XLI-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."

81 a 148 c 136 g 198 t
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Pred. No. 4.8e-63;
D; Mismatches 112
bp mRNA linear EST 28-
max cDNA clone GENOME SYSTEMS (
to SW:CGD1_ARATH P42751 CYCLIN
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                                                                                                      CCGCTGCCGCCGCGCCTCATGTCGGTTTCCTGCCTCTCCGACTACGAC¢TCCTCTGC
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GGCGAGGACTCCTCCGGAATCCTCTCCGGAGAGTCGCCGGAGTGCTCCTTCTCCGACATC
                                                                                                                                                                 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@rdsgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae;
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
Site_2: NotI; This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pT7T3-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE ID: Gm-c1043-4046"
/clone_lib="Gm-c1043"
/tissue_type-"Hypocotyl and Plumule, germinating seeds"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
/db_xref="taxon:3847"
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95.4%;
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                                                                                                                                                                                                                                                                                                                                                                       Length
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Harvey,N., Schurk
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Beck,C.,
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RESULT 9
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
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Public Soybean EST Project
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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/note="Vector: pT773Pac (Pharmacia); Site_1: EcoRI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The CDNA fragments were directionally cloned into the EcoRI. NotI restriction site of the pT773-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr.
                                                                                                                                                                                                                                                                                                                          /tissue_type="Hypocotyl and Plumule,
/lab_host="DH10B"
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/clone_lib="Gm-c1043"
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/db_xref="taxon:3847"
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                                                                           Hahn,M.G., Ojanen-Reuhs,T., Samac,D., T
Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula
oligogalacturonides of DP 6-20
                                                                                                                                Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                          University of Georgia 220 Riverbend Road, Athens, Tel: 706-542-4457
                                                            Unpublished (2001)
Contact: Michael G. Hahn
                                                                                                                                                                             EST
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BG647122.1 GI:13782234
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                  Fax: 706-542-4412
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hahn@ccrc.uga.edu
8e TIGR sequence n
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                      TGGGCCAAGTTGTCTAGAAACCTCAACATTTTTTAGAGGGTTTTTTGCAATTAAAAAATGA 1300
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Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the c
with 0.5 mg/ml oligogalacturonides (DP 6-20)
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
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/clone="pHOGA-15D4"
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                                                  CTTCAGATAGAAGGTGCCAAGTACATATTTGAGCCGAGAACAATTCGTAGGÅTGGAGCTA
                                                                                                                                GTTGCATGCTTGTCTTTGGCAGCAAAGATGGAAGAACCTCTTGTTCCATCTCTTGGAC
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                                CTTCAGGTTGAAGGCGCAAAGTATATATTTGAACCAAAAACTATCCAAAGAATGGAGTTT
                                                                                                GTTGCTTGCTTATCTTTAGCAGCAAAAATGGAGGAACCTCTTGTTCCCTTCC¢TTTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone info: please contact Research Genetics, Division tel 1-800-711-6195, email cdna@resgam as Seq primer: M13F-P
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BG88688
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Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and )
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40°C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."
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Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \mathtt{EST535463} P. infestans-challenged leaf Solanum tuberosum cDNA clone PPCAU06 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                For clone info: please contact Research Division tel 1-800-711-6195, email cdna@
                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cathy Ror
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potato.
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                                                                                                                                                                                                                                                                                                                                                            primer: M13F-R.
/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P.
                                                                                                                                                                   /clone_lib="P. infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
                                                                                                                                                                                                                                  /db_xref="taxon:4113"
/clone="PPCAU06"
                                                                                                                                                    /lab_host="SOLR"
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H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S. Holt,I.E. and Fraser,C.M.

ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolli
Unpublished (2000)
                                                                                                                                                                                                                                                                                  sequence.
BF520221
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Pred. No. 9.2e-45;
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  TATAAAAAGAAGAAATTAAATAGCTGGTTCTGGGTAGATGTTGACAAAAGGAAACTCAGAG
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University of Minnescta name: M277659e
TIGR sequence name: MTFCP93TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
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Fax: 651 649 5058
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8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
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trifolii"
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/cultivar="genotype A17"
/db_xref="taxon.3880"
/clone="pbSIL-22P18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jim Brandle Genomics and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001
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Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
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Stevia rebaudiana
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brandleje@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Landrace"
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                                                                                                                                                                                                Contact: Cathy Ronning
The Institute for Genomic Research
For Clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                          potato.
Solanum tuberosum
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EST.
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EST495740 CSTS
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                                                                                                                                                                                                                                                                                                                                                                                      Asteridae; euasterids I;
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                   /tissue_type="sprouting
/dev_stage="12-14 weeks
/lab_host="SOLR"
                                                                                                                                                                                  Location/Qualifiers
                                                                          /clone_lib="cSTS"
                                                                                           /clone="cSTS16P1
                                                                                                 /db_xref="taxon:4113"
/clone="csTS16P1"
                                                                                                                               /cultivar="Kennebec'
                                                                                                                                              /organism="Solanum tuberosum"
'note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:13615202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum
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DNA clone
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                                    from tubers"
harvest"
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and Baker,B.
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sequence,
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BASE COUNT
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Best Local Similarity 68.1%;
Matches 430; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 TYCCTGCCTCTCCGACCTACGACCTCCTCCGGGGAGGACTCCTCCCGGAATCCTCTCCGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AGAGTCGCCGGAGTGCTCCTTCTCCGACATCGACTCCTCACCTCCTCCGCCGTCGCCGAC 294
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                                                                                                                                                 535 GCCTCTGCAACCTTGTATCTGTTGCATGCTTGTCTTTGGCAGCAAAGATGGAAGAACCTCT 594
568 TATCCAAAGAATGGAGTTTCTTGTGCTGAGGATATTAGATTGGAGGCTCCGATCCATAAC
                       655 AATTCGTAGGATGGAGCTACTTGTTCTCGGTGTCTTAGATTGGAGGCTAAGATCAGTAAC 714.
                                                                                                 595
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                                                                                                                                                                                                                                                                                                                                 CGCCGTCAACTATATGGATCGGTTTTTGGATTCTCGCCGGTTGCCGGAAACAAATGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."

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Pred. No. 1e-36;
0; Mismatches 195; Indels
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Search completed: October 26, Job time: 2672 secs 2002, 00:25:39 οy 밁 δÃ 망 Q 밁 δÃ В Ş 밁 Q 밁 QΥ

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715 ACCACTTTGCTTCCTCGCTTTCTTTGCGTGCAAAGTAGAATTCAACTGGAACTTTTATCCG

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GTTCCTTATTTCCAGGGCAACAGAAATCATC 805

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sequence

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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           and is derived by
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(without alignments)
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-101-3988-1
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US-08-724-394A-21
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                                                                                INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
      Query Match
                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT: APPLICANT:
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: 703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESSPONDENCE ADDRESS:
CORRESSPONDENCE ADDRESS:
                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1800 Diag
CITY: Alexandria
STATE: VA
                                                                                                                                                                          TELEPHONE: (703)836-930
TELEFAX: (703)683-4109
TELEX: 899149
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US-08-738-367-8
US-08-7138-367-8
US-07-817-920-1
US-08-117-006-1
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US-08-216-594-1
US-07-781-355-1
US-09-156-425-1
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US-09-156-425-1
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US-08-885-469-1
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US-09-244-796-17
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Patent No. 567036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1193 AACGAACAATAATAAAAGAAGGGAAGAAAAAGAGAGGGAATAAGGTGGGCCAAGTTG 1252
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                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  TELEFAX:
                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                  TELEPHONE:
                                                                                                                                                                                        APPLICATION NUMBER:
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                                   899149
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1800 Diagonal Road,
                                                (703)836-9300
(703)683-4109
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30; Mismatches 145; Indels
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US-08-011-398B-1
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GENERAL INFORMATION:
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                                                                                                                                                   SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50% or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
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IMMEDIATE SOURCE:
                 ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
                                                                                  APPLICATION NUMBER: US/0: FILING DATE: 29 JAN 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1425 YYYYYYYYYGTACCAAATTC 1445
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 ACCTGTCGCGGTTCCAATCTC 383
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                             CITY: Boston
REGISTRATION NUMBER:
                                                    FILING DATE:
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                             02110-2804
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Best Local S
Query Match
Best Local Similarity
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                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            NAME: Paul T. CLGL. 30,162
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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nes 70; Conserv
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STRANDEDNESS: single
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                                                                              STRANDEDNESS:
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                                                               TOPOLOGY:
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                                                                                                                                                                     (617) 542-8906
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Pred. No. 0.016;
 Score 45.4; DB 1;
Pred. No. 0.016;
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                                                                                                                                                 Query Match
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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MEDIUM TYPE: 3.5" Di
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APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT IMPORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                  Local
                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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COMPUTER: II
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                                                                                                                     Similarity 63.1
70; Conservative
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IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOS (Version 5.0
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                                                                                                                  Score 45.4; DB Pred. No. 0.016; O; Mismatches
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RESULT 6 US-08-554-385-2

Sequence 2, Application US/08554385 Patent No. 6017692

ENERAL INFORMATION:

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Best Local Similarity 63.1
""" Conservative
                                                                                                                                                                                                                                               Sequence 1, Application US/08011398B Patent No. 5512473
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                           TITLE OF INVENTION: MAXINTERACTING PROTEINS AND RELATED TITLE OF INVENTION: MOLECULES AND METHODS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: NO. 601;
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                              APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTER
                                                                                                                                                                                                                                                                                                                                                   2307 CCCTCTCCCTTACCCTGGGAAGGCCTCTTGGAGACCTTACCCCTGGCTGTTTGGACTTTG 2366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEPAX: (617) 542-8906
                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
                                COUNTRY: U.S.A. ZIP: 02110-2804
                                                                  STATE:
                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                Boston
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                                                                 Massachusetts
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                                                                                              225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%;
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RESULT 8
US-08-464-051-1/c
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WOTGPERFECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NITMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                            APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/ACENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Roger Bren
APPLICANT: Antonis S.
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                    ZIP: 02110-2804
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    Application US/08464051
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SYSTEM: MS-DOS (Version 5.
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RESULT 9
US-08-462-498-1/c
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US-08-464-051-1
                                                             US-08-462-498-1
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Best Local :
Query Match 2.0%;
Best Local Similarity 66.0%;
Matches 64; Conservative
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TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                              NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/462,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2417
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MEDIUM TYPE: 3.5" D1
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APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
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CLASSIFICATION: 435
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STRANDEDNESS: sing
                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                    TELEFAX: (617) 542-8906
TELEX: 200154
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Local Similarity 66.0%;
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(617) 542-8906
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Score 44.2; DB 2;
Pred. No. 0.034;
0; Mismatches 33;
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RESULT 10
US-08-554-385-2/c
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RESULT 11
US-08-724-394A-20
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                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50% or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Roger Brent
APPLICANT: Antonis S. 2
TITLE OF INVENTION: MAN
TITLE OF INVENTION: MOI
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEFAX: 200154
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                                                                                                                                                                             Similarity
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MAX-INTERACTING PROTEINS AND RELATED
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                                                                                                                                                                Score 44.2; DB Pred. No. 0.034; 0; Mismatches
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                                                                                                                                                                                          DB 3;
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; Sequence 20, Application US/08724394A
Patent No. 5872237
; GENERAL INFORMATION:
: APPLICANT: Feder, John N.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                    27273
                                                                                                                                                                                                                                                                                             27153 TAAATAATTTGAATTATTTTAAAATAACTACCTAAAATTCCTAAATAATTACATAAATTA 27212
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ADDRESSEE: TOWNSEND and CREW LLP
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LENGTH: 246240 base pa
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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NAME: Fitts, Rence A.
REGISTRATION NUMBER: 35,136
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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LOCATION: 1..246240
OTHER INFORMATION: /no
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                                                                 GTAGAAGAATTTAATGTGATTTGTTCTTGTAACCTGTGATTCTGAAGGAAAGAATTGAGT 1573
                                                                                                                                 ATAGATTTTAAAATAAAATAAAAATAAATGCAATAAGGCCCCTAAATATCTGGCATCAT 27332
                                                                                                                                                                                                 TTTATGTTGGTGACTTATTAATATTGAGTTTGCAGAATTCACCTAGGGAAGAGGGATTTT 1453
                                                                                                                                                                                                                               TGCGGGCTGGATTTCAAAGTTTGCATTAATTACTTGGTGAAGGAGATGAAAG 1625
                                 TATAAATAATACAAGGTATATGATTCATGTGAGAATCAAGATTTGAGGATGAACATAAAT
                                                                                                 GCTATAAAGTAGAGAGCCAAAGAATATAAAAATATGAAATATTTTACCCACTCAAAAAAAC
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Wolff, Roger K.
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Sequences and Antibodies Thereto
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US-08-724-394A-21
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                  27153 TAAATAATTTGAATTATTTTAAAATAACTACCTAAAATTCCTAAAATAATTAAAATTA 27212
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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TITLE OF INVENTION: Sequences and Antibodies
NUMBER OF SEQUENCES: 31
 1514 GTAGAAGAATTTAATGTGATTTGTTCTTGTAACCTGTGATTCTGAAGGAAAGAATTGAGT 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                   Local Similarity 45.;
nes 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 01-OCT-1996
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OTHER INFORMATION:
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                                                                     GCGACATGTTACCGTGGGAGAGGAAATGAGAAGAAGAAGTGAAACACTGAACCAGGG 1513
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Wolff, Roger K.
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RESULT 13
US-08-724-394A-22
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION OF SEQ ID NO: 22:
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                                                                                                                     STRANDEDNESS:
TOPOLOGY: not
MOLECULE TYPE:
                                                                                                                                          1274 TAGAGGGTTTTTGCAATTAAAAATGACTTGAGTGAGGGTGTAGATTATAATAGTATATA 1333
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
1394 TITATGTTGGTGACTTAATATATTGAGTTTTGCAGAAATTCACCTAGGGAAdAGGGGATTTT 1453
                                                                                     1334 TATGATATATCTCTATCGTATATACTAAGAGAGTTTGATGGGGTTTGGAGTAATTTTTATT 1393
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94111-3834
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                                                   ТАТТАССТБААТАТТТАССТАЛАЛАТАЛАТАДАТТТАЛЛАТАЛАТАЛАТАЛАТАЛА 27272
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Tsuchihashi, Zenta
Wolff, Roger K.
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                                                                                                                                                                                                       Score 43.2; DB 2; Pred. No. 0.71;
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; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 8
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Best Local S
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APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes
FILE REFERENCE: A-524
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APPLICANT: Coats, Steven R.

APPLICANT: Bass, Michael B.

APPLICANT: Robinson, Murray O.

TITLE OF INVENTION: NO. 6165753el Cyclin E Genes and Proteins FILE REFERENCE: A-524

CURRENT APPLICATION NUMBER: US/09/222,851

CURRENT FILING DATE: 1998-12-30

EARLIER APPLICATION NUMBER: 09/092,770

EARLIER FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 1215

TYPE: DNA

ORGANISM: Human

US-09-222-851-8
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Sequence 8, Application US/09222851
Patent No. 6165753
GENERAL INFORMATION:
Search completed: October 26, 2002, 01:39:56 Job time: 294 secs
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Matches 131; Conserv
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## ALIGNMENTS

RESULT 1
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AC AAY:
XX AY
DT 21-i
XX Cyc
KW Cyclin delta-1; soybean; cell cycle; cell division; transgenic plant; herbicide; plant breeding. Glycine max. Soybean cyclin delta-1. 21-DEC-1999 AAY31894; AAY31894 standard; Protein; (first entry) 339 ₽

19-MAR-1999; 30-SEP-1999 W09948486-A2 99WO-US06047

23-MAR-1998; (DUPO ) DU PONT DE NEMOURS & CO E 98US-0078948

Cahoon RE, Klein TM, Odell JT, Orozco ¥

WPI; 1999-591036/50. N-PSDB; AAZ19958.

New isolated plant cyclin genes, used to develop products herbicides and for developing plant breeding programs for

Claim 6; Page 52-53; 68pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cr This is the deduced amino acid sequence of a corn cyclin delta-1 cc protein derived from the nucleotide sequence (see AAZ1958) of a cc contig composed of clones isolated from soybean Authority (TM) cc herbicide-sprayed and soybean root ear cDNA libraries. It crepresents the entire protein. The invention relates to isolated cc nucleic acid fragments (see AAZ1953-66) encoding cyclin A, cyclin cc delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see CC AAY31889-902). It also relates to the construction of chimeric genes cc encoding all or a portion of a cyclin, in sense or antisense cc encoding all or a portion of a cyclin, in sense or antisense cc elementation, where expression of the chimeric gene results in altered cc elements of the cyclin protein in a transformed host cell. This would cc have the effect of altering the regulation of cell division in those cc cells. The nucleic acid fragments may be used to express cyclins in cc plant cells to enhance cell tissue culture growth. The availability co f mucleic acid sequences encoding all or a portion of cyclins should cc enhance cell growth in tissue culture, increase the efficiency cof gene transfer and help provide more stable transformations. The construction of inhibitors of those enzymes that may be useful as constructions.
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                                                                                                                Cyclin delta-1; soybean; cell cycle; cell division;
                                                                                                                                          Soybean cyclin
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              30-SEP-1999
                                          WO9948486-A2
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                                                                                                                                                                                                                                                                                                                                                              VPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPET
                                                                                                                                                                                                                                                                                                         MRSSTVSSFSSSSTSFSLSCKRKLNNRLWVDDKGNSE
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                                                                                                                                                                                                                                                                                                                                     MRSSTVSSFSSSSSTSFSLSCKRKLNNRLWVDDKGNSE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                      max
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                                                                                                 plant;
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                                                                                                                                             delta-1 partial polypeptide
                                                                                                    herbicide; plant breeding
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Pred. No. 7.6e-185;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC protein derived from the nucleotide sequence (see AAZ1955) of a CC clone isolated from a soybean embryo cDNA library. It represents CC 95% of the entire protein. The invention relates to isolated CC nucleic acid fragments (see AAZ1953-66) encoding cyclin A, cyclin CC delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see CC AAY31889-902). It also relates to the construction of chimeric genes CC encoding all or a portion of a cyclin, in sense or antisense CC encoding all or a portion of a cyclin, in sense or antisense CC elevels of the cyclin protein in a transformed host cell. This would CC levels of the cyclin protein in a transformed host cell. This would CC levels of the cyclin protein in a transformed host cell. This would CC ells. The nucleic acid fragments may be used to express cyclins in CC cells. The nucleic acid fragments may be used to express cyclins in CC plant cells to enhance cell tissue culture growth. The availability CC of nucleic acid sequences encoding all or a portion of cyclins should CC to enhance cell growth in tissue culture, increase the efficiency CC of gene transfer and help provide more stable transformations. The CC proteins can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated plant cyclin gene
herbicides and for developing
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                                                                                                                                                                                CEGLRKEKVIGCYOLMOELVINNNORKLPLLKVLPQLRVTTTTTRMRSSTVSSF--SSSSS
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                                Protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%; score 1262; DB 20; 78.2%; Pred. No. 3.2e-130; tive 29; Mismatches 28;
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
                                                                                                                                                                                                                                                       Local 214;
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240 NEIPNW-SVVKP-ENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQLRVTT
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                                                                                      MSVSCLSDYDLLCGEDSSGILSGESP-ECSFSDIDSSPPPPSPTTEDCYSIASFIEHERN
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Pred. No. 1.2e
44; Mismatches
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1.2e-104;
hes 62;
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The present sequence is that of an isoform of maize cyclin D (CycD), a protein necessary for progression from G1 into S phase.

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RESULT 7
AAY79322
ID AAY7
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AC AAY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                          AAY79322;
                                                                                 AAY79322 standard; Protein; 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that are involved in cell cycle regulation. Also provides AAY79321-24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CycD RNA or CycD polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                       338 PAVCYHSSSTS----KRRRITERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PLLSDDC--VATLVEKEVEHMPAEGYLQKLQRRHGDLDLAAVRKDAIDWIWKVIEHYNFA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ---TEDCYSIASFIEHERNEVPGFEYLSRFQSRSLD---ANAREESVGWILKVHAYYGFQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDCAASVLLCAEDNAAILGLDDDGEESSWA---AAATPPRDTVAAAAATGVAVDGILTEF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 YD------LLCGEDSSGI--LSGESPECSFSDIDSSPPPPSPT------------43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKY 157
                                                                                                                                                                                                                                                                                                                                                                                       NNNQRKLPLLKVLPQLRVTTRTRMRSSTVSSFSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLTAVLSVNYLDRFLSTYEFPEGRAWMTQLLAVACLSLASKIEETFVPLPLDLQVAEAKF 179
                                                                                                                                                                                                                                                                              -----SSSTSFSLSCKRRKLNNRL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                              KGAEFVVFRPSEIAASVALAAIGECRS-SVI--ERAASSCKYLDKERVLRCHEMIQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFEGRTIKRMELLVLSTLKWRMHAVTACSFVEYFLHKLSDHGAPSLLARSRSSDLVLSTA
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                                                                                                                                                                                                                                                                                                                                ------KITAGSIVLKSAGSSISSVPQSPIGVLDAAACLSQQSDDATVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%; Score 502.5; DB 2: 34.0%; Pred. No. 1.9e-46; tive 60; Mismatches 99
                                                                                                                                                                                                                       357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
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QΥ

YD-----LLCGEDSSGI--LSGESPECSFSDIDSSPPPPSPT--

Query Match Best Local Matches

Local

al Similarity 33.8 130; Conservative

28.2%;

Score 496.5; DB 21 Pred. No. 8.8e-46; 0; Mismatches 100;

Indels Length 358;

95;

Gaps 43

11;

DB 21;

Sequence

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corrections in and texpression cassettes (including Zmcycli in sense or castettes), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or collseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises comprising a CycD polynucleotide linked to a promoter, and growing the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and cycD polynucleotide linked to a promoter, and cycD polynucleotide inked to a promoter, and cycD polynucleotide inked to a promoter, and cycD polynucleotide sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the cycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, cincrease the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, cassel, stalk, pollen, stamen) growth, produce organ ablation, creasel, stalk, pollen, stamen) growth, produce organ ablation, provide positive selection, increase plant regeneration, alter the time constitute selection, increase plant regeneration, alter the time that cells are arrested in G1 or G1 organ ablation and cell cycle, improve response to environmental stress including character or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in crease the number of seeds per pod or ear, alter the lag time in the cell creates 
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                                                                  seed development, provide hormone independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD kNA or CycD polypeptides. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of an isoform of maize cyclin D (CycD), a protein necessary for progression from G1 into S phase. CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle regulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 121-122; 134pp; English
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ARESULT 8
ANY 7932 3
ID AAY 7
XX AAY 7
XX AAY 7
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XX MA1z
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The present sequence is that of an isoform of malze cyclin D (CycD), a protein necessary for progression from G1 into S phase. CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AAX94581-84) and polypeptides (see AAX9479321-24) that are involved in cell cycle regulation. Also provider recombinant expression cassettes (including ZmcycD in sense or antisense orientation), host cells, transgenic plants (especially
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N-PSDB; AAZ94583.
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                                                                                                                                                                                                                                                                                             Claim 16; Page 124-125; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides encoding maize cyclin D isoforms related proteins and antisense RNA useful for control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                      regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 PAVCYHSSSTS----KRRMITRRL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGAEFVVFRPSEIAASVALAAIGECRS-SVI--ERAASSCKYLDKERVLRCHEMIQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFEGRTIKRMELLVLSTLKWRMHAVTACSFVEYFLHKLSDHGAPSLLARSRSSDLVLSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLLSDDC--VATLVEKEVEHMPAEGYLQKLQRRHGDLDLVAVRKDAIDWIWKVIEHYNFA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNNQRKLPLLKVLPQLRVTTRTRMRSSTVSSFSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLTAVLSVNYLDRFLSTYEFPEGRAWNTQLLAVACLSLASKIEETFVPLHLDLQVAEAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SSSTSFSLSCKRRKLNNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TEDCYSIASFIEHERNFVPGFEYLSRFQSRSLDAN---AREESVGWILKVHAYYGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDCAASVLLCAEDNAAILGLDDDGEESSWA---AAATPPRDTVAAAAAAT¢VAVDGILTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KITMGSIVLKSAGSSISSVPQSPIGVLDAAACLSQQSDDATVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tao Y, Gordon-Kamm WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0101551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US21946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gregory CA,
                                                                                                                                                                                                                                                                                                                                                                                    control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McElver
                                    in sense or
                                                                                                                                                                                                                                                                                                                                                                                 cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
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RESULT 9 AAY31897

AAY31897 standard; Protein;

388

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AAY31897; 21-DEC-1999

(first entry)

Corn

cyclin delta-2 partial

polypeptide

cell cycle; cell division;
plant breeding.

Cyclin delta-2; corn; maize; transgenic plant; herbicide;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or collseed Brassica) and antibody compositions. A claimed method of CC modulating the level of CycD protein in a cell comprises.

CC transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and cycD protein in the cell for a time sufficient to induct on the comprises.

CC cycD protein in the cell. The CycD protein is present in an amount contract of cells are real division, increase or decrease) the cclividing, improve transformation frequencies, alter cell growth, cc increase the growth rate, increase crop yield, alter plant chaight or size, enhance or inhibit organ (seed, root, shoot, ear, cc tassel, stalk, pollen, stamen) growth, produce organ ablation, compositive selection, increase callus induction, provide constitive selection, increase plant regeneration, alter the time cc that cells are arrested in Gl or GO phase or in a particular cell cycle, improve response to environmental stress including cells increase the number of pods per plant, concease the number of pods per plant, concease the number of cells time in cc seed development, provide hormone-independent cell growth, or cc concease the number of cells in bioreactors. The level of cycD protein in the cells is transiently modulated by introducing cyclp RNA or CycD polypeptides. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
    346
                                         303
                                                                                                                        276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVSCLSDYD-----LLCGEDSSGIL-------SGESPECSFSD---IDSSP
SHGPPGSSSSSSTS-PVTSKRRKLASR
                                                                                                                                                                                                   NIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQEL
                                                                                                                                                                                                                                           VFEAKTVQRMELLVLTTLNWRMHAVTPFSYVDYFLNKLSNGGSTAPRSCWLLQSAELILR
                                                                                                                                                                                                                                                                                                                        PLTAYLAVNYLDRFLSLSEVPDGKDWMTQLLAVACVSLAAKMEETAVPQCLDLQVGDARY 169
                                                                                                                                                                                                                                                                                                                                            PLTAYLAVNYMDRELDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKY 157
                                                                                                                                                                                                                                                                                                                                                                                                     ----PQSEEC--VAGLVERERDHMPGPCYGDRLRGGGGCLCVRREAVDWIWKAYTHHRFR
                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQ
                                       SSTVSSFSSSSSTSFSLSCKRKLNNR 329
                                                                                 ASSAAIDGDATVPPKSARRRSSPVPVPVPVPVPQSPVGVLDAAACLSYRSEEAATATATSAA
                                                                                                                                                                AARGTGCVGFRPSEIAAAVAAAVAGDVDDADGV--ENA--CCAHVDKERVLRCQEAIGSM
                                                                                                                                                                                                                                                                  MAPSC ---YDAAASMLLCAEEHSSILWYDEEEEELEAVGRRRGRSP--GYGDDFGADLFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                        --INNNQRKLPLLKVLPQLRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.7%; Score 470; DB 21; 33.6%; Pred. No. 8.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Mismatches
      371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                        ----TTRTRMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein derived from the nucleotide sequence (see AAZ19961) of a clone from an embryo leaf cDNA library. It represents 94% of the full-length protein. The invention relates to isolated nucleic full-length protein. The invention relates to isolated nucleic acid fragments (see AAZ19953-66) encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see AAX1889-902). It also relates to the construction of chimeric genes encoding all cor a portion of a cyclin, in sense or antisense orientation, where expression of the chimeric gene results in altered levels of the cyclin protein in a transformed host cell. This would have the cyclin protein in a transformed host cell. This would have the cells to enhance cell tissue culture growth. The availability of cells to enhance cell tissue culture growth. The availability of the onhance cell growth in tissue culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets to facilitate design and/or identification of the interference convenes that may be used for a protein constitution.
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 56-57; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated plant cyclin genes, used to develop products for use herbicides and for developing plant breeding programs \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentification of inhibitors of those enzymes that may be useful as
                                                                                                                                                                  157
                                                                                                                                                                                                  110
286 MASSAAIDDATVPPKSARRRSSPVPVPQSPVGVLDAAPCLSYRSEEAATATATATSAASH
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                                                                                                                                                                                                                                                                                                  38
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                                                                                                                                                                                                                                                                                                                                                                  1 MSVSCLSDYD-----LLCGEDSSGIL-------SGESPECSFSD---IDSSP
                                                                                                                                                   PLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEG-AK
                                                                                                                                                                                                                                                                                                                                  MAPSC---YDAAASMLLCAEEHSSILWYEEEEEELEAVGRRSGRSP--GYGDDFGADLFP
                                                                                                                                  YVFEAKTVQRMELLVLTTLNWRMHAVTPFSYVDYFLNKLNNGGSTAPRSCWLLQSAELIL
                                                                                                                                                                                                PLTAYLAVNYLDRFLSLSEVPDCKDWMTQLLAVACVSLAAKMEETAVPQCLDLQEVGDAR
                                                                                                                                                                                                                                                                  ----PQSEEC--VAGIVERERDHMPGPCYGDRLRGGGGCLCVRREAVDWIWKAYTHHRFR
                                                                                                                                                                                                                                                                                                 PPPSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQ
                                 LV---
                                                                RAARGTGCVGFRPSEIAAAVAAAVAGDVDDADGV--ENA--CCAHVDKERVLRCQEAIGS
                                                                                                SNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%;
34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                 -- INNNQRKLPLLKVLPQL-----RVTTRTRMRSSTVS-
                                                                                                                                                                                                                                                                                                                                                                                                 Score 467; DB 20;
Pred. No. 1.8e-42;
62; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                       25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                               28-MAY-1999;
01-JUN-1999;
                                                                                              20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG47103 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG47103;
                                                                                                                                                                                                                                                                                                                 06-APR-1999
                                                                                                                                                                                                                                                                                                                         01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2000
                                               07-JUN-1999;
08-JUN-1999;
                                                                                                                                                14-MAY-1999;
18-MAY-1999;
                                                                                                                                                                                                       06-MAY-1999;
                                                                                                                                                                                                                        04-MAY-1999
05-MAY-1999
                                                                                                                                                                                                                                                 30-APR-1999;
                                                                                                                                                                                                                                                       23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                                       21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                        16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                                        08-APR-1999;
                                                                                                                                                                                                                                                                                                                                 29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 GAPGSSSSSSTSPVTSKRRKLASR 369
                                                                04-JUN-1999;
                                                                         03-JUN-1999;
                                                                                                                                                                14-MAY-1999;
                                                                                                                                                                         14-MAY-1999;
                                                                                                                                                                               14-MAY-1999;
                                                                                                                                                                                        11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 -- SFSSSSSTSFSLSCKRKLNNR 329
                                10-JUN-1999;
                                        10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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243
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RESULT 12 17-0CT-2000 AAG23946; AAG23946 standard; Protein; (first entry) 367 ξ

Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter; Arabidopsis thaliana protein fragment SEQ ID NO: 27438.

termination sequence

EP1033405-A2 Arabidopsis thaliana

06-SEP-2000

25-FEB-2000; 2000EP-0301439 9908-0121825

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RESULT 13 AAG23337; ID AAG23337; XX AC AAG23337; XX PT 17-OCT-2000 (first entry) XX Arabidopsis thaliana protein fragment SEQ ID NO: 26608. XX Protein identification; signal transduction pathway; metabolic pathway; KW hybridisation seasay; genetic mapping; gene expression control; promoter; KW termination sequence. XX PED1033405-A2. X	PR 26-OCT-1999; 99US-0161360.  PR 28-OCT-1999; 99US-0161920.  PR 28-OCT-1999; 99US-0161942.  Query Match  23.9%; Score 419.5; DB 21; Length 367;  Best Local Similarity 35.7%; Pred. No. 2.8e-37;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Gaps 7;  Matches 107; Conservative 57; Indels 31; Indels 35; Indels 3
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                                                        protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
                                                                                                                                                       AAG53864 standard; Protein; 361
06-SEP-2000
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                    EP1033405-A2.
                                     Arabidopsis thaliana.
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                                                                                             thaliana protein fragment SEQ ID NO: 68617.
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                                      DEAVYQSQLMTLLKVDSEKVNKCY----ELVLDHSPSKKRMMNWMQQPASPIGVFDASFS
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Search completed: October 23, 2002, 14:38:10 Job time : 36 secs

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408	399	398	460	415	484	446	473	493	398	471	419	341	460	449	454
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cyclin B - common	cyclin B2 - chicke	cyclin B2 - mouse	probable mitotic c	cyclin A2 - Africa	cyclin a2-type, mi	mitosis-specific c	mitosis-specific c	cyclin, A-type - c	hypothetical prote	cyclin B1 - yeast	cyclin 2 - rice	mitosis-specific c	protein F2D10.10 [	cyclin - common to	mitosis-specific c

## ALIGNMENTS

C:Accession: A96725
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor, R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Rature 408, 816-820, 2000
Rature 408, 816-820, 2000
Rature 408, 816-820, 2000
Rature 408, 11, J.H.; Li, Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Lit, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Hitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Reference number: A86141; MUID:21016719 hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001 A;Cross-references: GB:AE005173; NID:g2194121; PIDN:AAB61096.1; GSPDB:GN00141 A; Molecule type: DNA A; Residues: 1-339 <STO> A;Status: preliminary 122 TSGWPMQLLAVACLSLAAKMEEILVPSLFDFQVAGVKYLFEAKTIKRMELLVLSVLDWRL 1 MSVSCLSDYDLLCGEDSSGILSGESP-ECSFSDIDSSPPPPSPTTEDCYSIASFIEHERN 59 RSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAA 239 NEIPNW-SVVKP-ENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQLRVTT 297 RSVTPFDFISFFAYKIDPSGTFLGFFISHATEIILSNIKEASFLEYWPSSIAAAAILCVA Similarity Conservative 58.6%; Score 1030; DB 2; Length 339; 63.3%; Pred. No. 4.1e-85; 44; Mismatches Indels 18; Gaps 299 181 179 241 7;

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RA-~-SSTLTRPSDESSFSSSSSPCKRKLSGYSWVGDE 334

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cyclin D-like protein - red goosefoot
C;Species: Chenopodium rubrum (red goosefoot)
C;Species: Chenopodium rubrum (red goosefoot)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T09961
R;Renz, A.; Fountain, M.; Beck, E.
submitted to the EMBL Data Library, December 1996
A;Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotr
A;Reference number: Z16906
A;Accession: T09961
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <RENV
A;Cross-references: EMBL:Y10162; NID:e1014005; PID:e290219
A;Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl
C;Genetics:
A;Gene: cycl1
C;Keywords: cell cycle control; cell division control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclin delta-1 - Arabidopsis thaliana
N;Alternate names: cyclin D homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
C;Accession: S51650
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A; Residues: 1-334 <SON>
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A;Description: A family of cyclin D homologs from plants differentially controlled
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C;Keywords: cell cycle control; cell division control
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                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVPGFEYLSREQSRSLDANAREESVGWILKVHAYYGEQPLTAYLAVNYMDRELDSRRLPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTRMRSSTVSSFSSSSSTSFSLSCKRRKLNNRLWVDDK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIPNW-SVVKP-ENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQLRVTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSVTPFDF1SFFAYKIDLRVPFSGSL-SPMLQS1LSNIKEASFLEYWPSSIAAAAILCVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA---SSTLTRPSDESSS----PCKRRKLSGYSWVGDE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NELPSLSSVVNPHESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTP--KVIAKLRVSV
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  Conservative
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                          26.4%; Score 463.5; 31.7%; Pred. No. 6.1
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44; Mismatches 67;
  66;
  Mismatches 116;
                          6.1e-34;
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                                                 DB 2;
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  Indels
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Gaps
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FRPSEIAAAAAVSVSIS-GETECIDEEKALSSLIYVKQERVKRCLNLMRSLTGEENVRGT 298 YWPSCIAAAAILTAANEIPNWSVYKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKL 284 KRMELLVVTTLNWRLQALTPFSFIDYFVDKI--SGHVSENLIYRSSRFILNTTKAIEFLD RRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLA

239

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122 MNYLDRFLTSYELPKDKDWAAQLLAVSCLSLASKWEETDVPHIVDLQVEDPKFVFEAKTI 181

105 VNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTI 164

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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable cyclin D [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A; Residues: 1~361 <STO>
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                                                                                                                                                                                                                                                                                                                                                     Genetics
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 DWIHKVQSHYNFGPLCVYLSVNYLDRFLSAYELP-GKAWMMQLLGVACLSLAAKVDETDV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 NSAHSSPASAPPPKRRKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 -----KRRKLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 LIFQAIQLILSTIKGIDLMEFRPSEIAAAVAISVTQQT---QIVEFTDKAFSFLTDHVEK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 LISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVK-PENAESW-CEGLRK 262
  64
                                                    45
                                                                                                                                                     10 DLLCGEDS-SGILSGESPECSF-----SDID------SSP----PPPSPTT 44
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                                                                                                   4 NLACGETSESWIIDNDDDDINYGGGFTNEIDYNHQLFAKDDNFGGNGSIPMMGSSSSSSSS
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ED--RIKEMLVREIEFCPGTDYVKRLLSGDLDLSVRNQALDWILKVCAHYHFGHLCICLS
                                                 EDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLA 104
                                                                                                                                                                                                       120;
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Pred. No. 7.9e-33;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                    Length 361;
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  121
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cylin delta-3 - Arabidopsis thaliana
N;Alternate names: cyclin D homolog; protein F28A23.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05420; S51652
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.;
submitted to the Protein Sequence Database, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclin delta-2 - Arabidopsis thaliana
N;Alternate names: cyclin D homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 25-Apr-1997
C;Accession: S51651
R;Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
                      A;Experimental source: cultivar Columbia; BAC clone F28A23
R;Son1, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
submitted to the EMBL Data Library, December 1994
A;Bescription: A family of cyclin D homologs from plants differentially controlled A;Reference number: $51650
A;Accession: $51652
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A;Description: A family of cyclin D homologs from plants differentially controlled by gr
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C;Keywords: cell cycle control; cell division control
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A; Residues: 1-383 <SON>
A; Cross-references: EMBL: X83370
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A; Accession: S51651
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A; Residues: 1-376 <BEV>
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQLRVT†RT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 VSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 PLLKVLPQLRVTTRT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRLLSGDLDLSVRNQALDWILKVCAHYHFGHLCICLSMNYLDRFLTSYELPKDKDWAAQL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSQ--EQARVAVRAVPASPVGVLEATCLSYRSEERTVESCTNSSQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHQLFAKDDNFG-GNGSIPMMGSSS-----SSLSED--RIKEMLVREIEFCPGTDYV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDYFVDKI--SGHVSENLIYRSSRFILNTTKAIEFLDFRPSEIAAAAAV$VSIS-GETEC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.3%; Score 444; DB 2; 35.4%; Pred. No. 3.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RMRSSTVSSFSSSSTS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length
                                                                                                                                                                                                                                                                                                                                                   K.; Dauner, D.; Herzl,
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A;Residues: 1-287,'C',289-370,'R',372-376 <50N
A;Cross-references: EMBL:X83371; NID:g603508;
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: protein F3A4.150
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 158/3; 226/1; 269/3
A;Introns: 158/3; 226/1; 269/3
A;Note: F28A23.80
C;Keywords: cell cycle control; cell division control
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A; Introns: 157/3; 225/1;
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A;Experimental source: cultivar Columbia; BAC clone F3A4
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                                                                                                                                                                                                                                                                        A; Note: F3A4.150
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A; Residues: 1-361 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T45860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 SSKKRKSHDSSSSLNSPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 DPFDPLSYQTNLLGVLNLTKEKVKTCYDLILQLPVD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 TPISFVDHIIRRLGLKNNAHWDFLNKCHRLLLSVISDSRFVGYLPSVVAAATMMRIIEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 TPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 WMLQLVSVACLSLAAKVEETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHLI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 WPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSV 182
66 YLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPL 125
                                                                        49 LSDHDMLWDDDELSTLISKQEPCLYDEI-----LDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 DDVYLS-----TDRKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQRDKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 DALYCEEEKWDDEGEEVE-ENSSLSSSSPFVVLQQDLFWEDEDLVTLFSKEEEQGLSCL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 DLLCGEDSSGILSGESPECSFSDIDSSPPPPSPTTEDCY----SIASFIEHERNFVPGF 64
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                                                                                                                    6 LSDYDLLCGEDSSGILSGESPECSFSDIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFE 65
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                                                                                                                                                                     109;
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.;
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                                                                                                                                                                23.4%; Score 411; DB 2; 31.4%; Pred. No. 3.2e-29; ative 59; Mismatches 119
                                                                                                                                                                                                                                                                                               268/3
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                                                                                                                                                                     Mismatches 119; Indels
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                                                                                                                                                                                                                 Length 361;
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81 FL------VLCREKALDWIFKVKSHYGFNSLTALLAVNYFDRFITSRKFQTDKPWMS 131

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A;Cross-references: G
C;Genetics:
A;Gene: AT4g03270
A;Map position: 4
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A;Cross-references: EMBL:X888864; NID:g1150931; PIDN:CAA61334.1; PID:g1150932 C;Genetics: A;Note: cycMs4
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A;Accession: E85041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable D-type cyclin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: E85041
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A; Residues: 1-302 <STO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LLSFHFQKEKPWMIQLVAVTCISLAAKVEETQVPLLLDLQVQDTKYVFEAKTIQRMELLI 201
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  264
                                                                                                                                                                                                                                                                                                                                             117 LPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 SYLATATMLHYIDQIEQ----SDDNGVDYKNQLLNYLKISKEKYDECYNAILHLINANN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 LSTLKWKMHPYTTHSFLDHIIRRLGLKTNLHWEFLR----RCENLLLSVLLDSRFVGCVP 257
                                                286 LLKVLPQLRVTTRTRMRSSTVSSFSSSSSTSF--SLSCKRKLNNR 329
                                                                                                                                               233 AAILTAANEI-----PNWSVVKPENAESWCEGLRKEKVIGCYQLMQE--LVINNNQRKLP 285
                                                                                                                                                                                                  151 WRMRSVTPFSFLAFFISLFELKEEDPLLLKHSLKSQTSDLTFSLQHDISFLEFKPSVIAG
                                                                                                                                                                                                                                              177 WRLRSVTPLCFLAF----FACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAA 232
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                                                                                                                                                                                                                                                                                                 94 MPQSKPWILKLISLSCVSLSAKMRKPDM-SVSDLPVEGE--FFDAQMIERMENVILGALK 150
                                                                                                                                                                                                                                                                                                                                                                                             35 EFQHMPSSHYFHSLKSSAFLLSNRNQAISSITQYSRKFD-DPSLTYLAVNYLDRFLSSED 93
                                                                                                                                                                                                                                                                                                                                                                                                                                              57 ERNEVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRR 116
                                                                                            AALLFASFELCPLQFPCFS----NRINQCTYVNKDELMECYKAIQERDIIVGENEGS--
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--TETAVNVLDQQFSSCESDKSITITASSSPKRKTSTR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:NC_001268; NID:g7270197; PIDN:CAB77812.1; GSPDB:GN00140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%; Score 340.5; DB 2; 32.5%; Pred. No. 5.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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hypothetical protein F19F18.120 - Arabidopsis thaliana

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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A96141; MUID:21016719

A;Accession: A96803
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                                           A; Map position: 1
C; Superfamily: cyclin
                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable mitotic cyclin a2-type [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: A96803
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A; Introns: 83/1; 112/1; 212/1; 261/3
A; Note: F19F18.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AL035605
A; Experimental source: cultivar Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the Protein S
A; Reference number: Z15382
A; Accession: T04720
A; Molecule type: DNA
                                                                                                        C; Genetics:
                                                                                                                             A;Cross-references: GB:AE005173; NID:g11079479; PIDN:AAG29191
                                                                                      A; Gene: F2P24.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-321 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SVACLSLAAKHEERIVPGLSQYP-QDHDFVFKPDVIRKTELLILSTLDWKMNLITFFHYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 ASGSGAKRRLSFDDSDQSS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 MRSSTVS---SFSSSSSTS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 EIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQLRVTTRTR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 AFFACKV--DSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TLPSKTTSSSDRLIAIDWILTVHKNKIWVPTSNSLHCNLILRSVSPQKIHRYETWAMRLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 --- SRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRIPETNGWPLQLV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LCHESESSL--NEDDDETIERSDKQEPHFTTTIDDEDYVADLVLKEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LCGEDSSGILSGESPECSFSDIDSSPPPPSPTTEDCYSIASFIEHERN†VPGFEYLSRFQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLTREEIANKFGSISWWTSNENENVYLCYQ--RTLEIEERKHMTP----FPEIAVSREPP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYFLAKISODNHSVSKDLVLLRSSDSLLALTKEISFTEYROFVVAAVTTILLASSSTSSDI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%; Score 276; DB 2; Length 321; 26.3%; Pred. No. 4.2e-17;
      14.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Columbia;
    Score 247;
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    DB
    2;
    Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LRFE 60
                                                                                                                             .|1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                     S.; White, O.; Alonso
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hypothetical protein T7H20.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T44032 C;Accession: T44032 R;Bevan, M.; Peters, S;A.; van Staveren, M.; Dirkse, W.; Stiekema, W.: Ranco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 5
A; Introns: 87/3; A; Note: T7H20.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-341 (BEV)
A;Cross-references: EMBL:AL162508
A;Experimental source: cultivar Columbia; BAC clone T7H20
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T48232
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 SESSDSVSGY 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 DTELLQSDDS---LLCSSPALS---LDASPTQSDPSISTHDSLTNHVVDYMVESTTDDGN 155
                                                                                                                                                                                                         122 GWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 SFSSSSSTSF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 ATLEHYTSYRAKHMEACVKNLLQLC---NEK---LSSDVVAIRKNTSLQQRSFVPRHYRK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GTFIRFLISRATEIIVSNIQEAS-----FLAYWPSCIAAAAILTAANEI-PNWSVVKPEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 CVP-----QVEDFCYITDNTYLRNELLEMESSVLNYLKFELTTPTAKCFLRRFLRAAQGR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 LVPSLLDLQIEGAKYIFEPRTIR----RMELLVLGVLDWRLRSVTPLCFLAFFACKVDST 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 LIDWLYEVAEEYRLSPETLYLAVNYYDRYLTGNAINKQN----LQLLGVTCMMIAAKYEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 DDDDDEIVNIDSDLMDPQLCASFACDIYEHLRVSEVNKRPALDYMERTQS-SINASMRSI 214
                                                                                                                                                                                                                                                                                  61 HGDKFVEFFVSKKL-TDYRFHAFQWLIQTRSRLNLSYETVFSAANCFDRFVYMTCCDEWT 119
                                                                                                                                                                                                                                                                                                                                                62 PGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 DLLCGED--SSGILSGESPECSFSDIDSS-----PPPPSPTTEDCYSIASFIEHERNF-V 61
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                                                                                                                                                                                                                                                                                                                                                                                                                          3 NLLCEESWPASPLTPEPLPNFRHRSHDNDVVKMYPEIDAATMEE--AIAMDLEKELCFNN 60
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VTSYTFSQTLVSKIGMVGD-~HMIMNRITNHLLDVICDLKMLQYPPSVVATAAI-~----
                                                                                                                                       NWMVELVAVTSLSIASKFNEVTTPLLEELEMEGLTHMFHVNTVAQMELIILKALEWRVNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ch 13.9%; Score 244; DB 2; Length 341; Similarity 26.6%; Pred. No. 3.5e-14; Conservative 56; Mismatches 128; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116/3; 215/1
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8; Mismatches 128
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231
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242 IPNWSVVKP----ENAESWCEGLRKEKVIGCYQLMORI,VTNNNODV

ls DAN : :
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-456 <ren> A;Cross-references: GB:U10076; GB:U10077; NID:g516549; PIDN:AAA20237.1; PID:g516550; GB C;Superfamily: cyclin 12 58. Score 220: DB 2: Length 456:</ren>
C;Accession: C57742 R;Renaudin, J.P; Colasanti, J.; Rime, H.; Yuan, Z.; Sundaresan, V. R;Renaudin, J.P.; Colasanti, J.; Rime, H.; Yuan, Z.; Sundaresan, V. Proc. Natl. Acad. Sci. U.S.A. 91, 7375-7379, 1994 A;Title: Cloning of four cyclins from maize indicates that higher plants have three str A;Reference number: A57742; MUID:94316698 A;Accession: C57742
RESULT 15 C57742 C57741 - maize Cyclin II - maize C;Specias: Zea mays (maize) C;Date: 23-Feb-1996 *sequence_revision 23-Feb-1996 *text_change 16-Jul-1999
QY 244 NWSVYKPENAESWCEGLRKEKVIG 267 :::   : : : : : : : : : : : : : : : : :
OY 195 VDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIP 243
Qy 144 VPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTELCELAFFACK 194
QY 84 VGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVAGLSLAAKMEEPL 143 :  :::
QY 29 SESDIDSSPPPDSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREES 83      ::  :
Query Match 13.0%; Score 228; DB 2; Length 502; Best Local Similarity 29.2%; Pred. No. 1.6e-12; Matches 77; Conservative 42; Mismatches 103; Indels 42; Gaps 10;
: 1-50; ference tal se tal se czwaw tly: c
Plant Mol. Biol. 37, 121-129, 1998 A;Title: Isolation and characterization of a functional A-type cyclin from maize. A;Reference number: 214713; MUID:98281580 A;Accession: T02746 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ
RESULT 14 T02746 Cyclin A-like protein CYCZM2W - maize Cyspecies: Zea mays (maize) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999 C;Accession: T02746 R:H41eh, W.L.: Wolniak, S.M.
Db 232WILMEDKVCRESIMNLFEQNHKEKIVKCVDGMKNRDIDHQSSR 274

Search completed: October 23, 2002, 14:39:31 Job time : 19 secs

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CG2B_ARTW
CGB2_CHICK
CGBB_ARATW
CG1B_MEDVA
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CG1B_MOUSE
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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	P32943 sacc	P51986 chlo	P39948 rat1	Q61456 mus	P10815 schi	P30279 home	P37881 mesc	Q04827 rati	P30280 mus	P43449 gall	P13351 xeno
cetulus	saccharomyc	orohydra	tus norv	musculu	izosacch	o sapien	ocricetu	tus norv	musculu	gallus gall	opus lae

## ALIGNMENTS

RA R	
	ID GCD1_ARATH STANDARD; PRT; 335 AA.  AC P42751; 004525; DT 01-NOV-1995 (Rel. 32, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 01-MAR-2002 (Rel. 41, Last annotation update) DE Cyclin delta-1. GN CYCD1 OR AT1670210 OR F20P5.7. OS Arabidopsis thaliana (Mouse-ear cress).  OC EUKarvota; Viridialiantae: Streptophyta: Embryophyta: Tracheophyta:

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Pfam; PF02984; cyclin_C; 1.
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PROSITE; PS00292; CYCLINS; 1.
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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CYCD2 OR AT3622490 OR F14M13.11.
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                                                                                                                                                                                                                     STRAIN-CV. LANDSBERG ERECTA; TISSUE-Seedling;
MEDLINE-95210930; PubMed-7696881;
Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
"A family of cyclin D homologs from plants differentially controlled
                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnollophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P42752;
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                                                                                                                                                    protein interaction motif."; Plant Cell 7:85-103(1995).
                                                                                                                                                                                                 by growth regulators and containing
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                                                 Submitted (MAR-1998)
                                                                       Murray J.A.H.;
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1e-86;
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01-NOV-1995 (Rel. 32, 0
15-DEC-1998 (Rel. 37, 1
16-OCT-2001 (Rel. 40, 1
Cyclin delta-3, 1
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., To Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldbl Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Uma Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Uma Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T. Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Goodman H.M., Somerville C.R., Copenhaver S.L., Fraser C.
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pfam; PF02984; cyclin_C; 1
SMART; SM00385; CYCLIN; 1.
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PROSITE; PS00292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Multigene fam

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Cyclin; Cell cycle; Cell division; Multigene fam
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EMBL; AC006592: AAD22252 1.
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CTCD3 OR AT4G34160 OR F28A23.80.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
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D2F CRC64;
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Embryophyta; Tracheophyta;

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RA Harris B., Ansorge W., Errandt R., Entlan K.-U., "Ently N., Ra Harris B., Ansorge W., Errandt R., Entlan K.-U., "Ently N., Ra Herits B., Ansorge W., Errandt R., Ridley M., Mueller M., Rader R., Mache R., Mueller M., Rader M., Welchselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Rader M., Welter B., Mache R., Mueller M., Rader M., Welter H., Ridley P., Ra Holzer B., Dorteelle D., Perez-Alonso M., Boutry M., Bancroft I., Rader Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Ra Harlis B., Periter S., Wan Ger Schweren J., Grymonprez B., Chuang Y. J., Vandenbussche F., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirke W., Rader B., Berneiser S., Hempel S., Feldpassch M., Lamberth S., Vah den Daele H., Raderen B., Brandt A., Peters S., van Staveren M., Dirke W., Rader B., Berneiser S., Hempel S., Feldpassch M., Lamberth S., Vah den Daele H., Ra Mocijman P., Klein Lankhorst R., Rose M., Hall J., Koetter P., Ra Mocijman P., Klein Lankhorst R., Rose M., Hall J., Kay M., Lennard N., McLay K., Mayes R., Ra Montagu M., Rogers J., Cronin A., Quall M., Bray-Allen S., Ra Van Montagu M., Rogers J., Cronin A., Quall M., Bray-Allen S., Ra Van Montagu M., Rogers J., Cronin A., Quall M., Bray-Allen S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmanh S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmanh S., Herzi A., Raber E., Petrager C., Wonfort A., Casacubert A., Ra Aberlo C., Puchs M., Fartmann B., Granderath K., Dauner D., Herzi A., Massenet O., Quigley F., Clabauld G., Mendlein A., Felber R., Ra Merisia D., Haase D., Lencke K., Mewes H., W., Tonnos S., Tacon D., Jesse T., Ra Merisia D., Haase D., Lencke K., Mewes H., W., Tonnos S., Tacon D., Jesse T., Ra Merisia D., Haase D., Lencke K., Mewes H., W., Stocker S., Belek C., Ra Merisia D., Miller R., Gotter S., Schotz K., Habermann K., Ra Merisia D., Miller R., Stocker S., Belek C., Peter S., Marces J., Peter S., Marces J., Peter S., Dante M., Petin M., Johnson D., Ra Merisia D., Miller R., Stocker S., Scholz V., Meris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
"A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mayer K.F.X., Schueller C., Wambutt R. Pohl T., Duesterhoeft A., Stiekema W.,
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                                                                                                                          Nature 402:769-777(1999).
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  18
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X MEDILINE-94148008; PubMed-8313906;
X MEDILINE-94148008; PubMed-8313906;
A Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
A Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
T "Patterns of cell division revealed by transcriptional regenes during the cell cycle in plants.";
I EMBO J. 13:616-624(1994).
C -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADII C (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADII C AND ARE ABRUPTLY DESTROYED AT MITOSIS.
C -1- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KIN A SERINE/THREONINE KINASE HOLDENZYME COMPLEX. THE CYCLINAMITY: SUBSTRAYE SPECIFICITY TO THE COMPLEX.
-1- DEVELOMMENTAL STAGE: ACCUMULATES STEADILY DURING G2 A ABRUPTLY DESTROYED AT MITOSIS.
C -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB S
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Pfam; PF02984; cyclin, C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell divi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
G2/mitotic-specific cyclin 2.
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EMBL; AL161584; CAB80133.1;
InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antirrhinum majus (Garden snapdragon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Pred. No. 6.9e-31;
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pfam; pF02984; cyclin_C; 1.
sMART; SM00385; CYCLIN; 2.
pR0SITE; pS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
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                                        Shiraki T., Yamashita K., Nishitani H., Nishimoto T.;
Shiraki T., Yamashita K., Nishitani H., Nishimoto T.;
Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT (MITOSIS) TRANSITION.

-I- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IM SUBSTRATE SPECIFICITY TO THE COMPLEX.

-I- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND ABRUPTLY DESTROYED AT MITOSIS.
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01-OCT-1994 (Rel. 30, Last
16-OCT-2001 (Rel. 40, Last
G2/mitotic-specific cyclin
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01-OCT-1994
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTA---ANEIPNWSVVKPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIWAPEVNDLVCISDGSYSNE--QVLRMEKKILGALEWYLTVPTPYVFLVRFIKASLPDS
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                           BELONGS TO THE CYCLIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
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27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation update)
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Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E6E4C037C98880A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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                           CYCLIN AB
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                           SUBFAMILY
                                                                                                                           IMPARTS
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RESULT 6
CG2B_MEDS
ID CG2B
DT 01-1
DT 01-1
DT 01-1
DT 01-1
DE G2/
OS Med
OC Euk
OC Euk
OC Spe
RN (1)
RN (1)
RN (1)
RA H1
RA H1
RA GC
CC
CC
CC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00134; cyclin; 1.

pfam; PF02984; cyclin_C; 1.

SMART; SM00385; CYCLIN; 2.

PROSITE; PS00292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Mitosis.

SEQUENCE 397 AA; 45278 MW; 247DBAA412E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                     MEDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000553; Cyclin.
            SEQUENCE FROM N.A.
MEDLINE-93104677; PubMed-1307238;
Hirt H., Mink M., Pfosser M., Boegre L.,
Gartner A., Dudits D., Heberle-Bors E.;
                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                        CG2B_MEDSA
                                                                                                                                                                                NCBI_TaxID=3879;
                                                                                                                                                                                                                                                                                                                                                                                            373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSVACLSLAAKMEEPLVPSLLDLQIEGAKYI----FEPRTIRRMELLVLGVLDWRLRSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCQAFSDALL----CKIEDIDNEDWENPQLCSDYVKDIYQYLRQLEVLQSINPHF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCGEDSSGILSGESPECSFSDIDS----SPPPPSPTTEDCYSIASFIEHERNFVPGFEYL
                                                                                                                                                                                                                                                                                                                                                                                            LKISTIPQLNSKTIKDLAS
                                                                                                                                                                                                                                                                                                                                                                                                                     LRVTTRTRMRSSTVSSFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                VLGQGKWNL-----KQQYYTGYMETEVLEVMQHMAKNVVKVNENLTKFIAVKNKYASSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EI--PNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLHFLRRASKAGEVDVEQHTLAKYLME-----LTLIDYDMVHYHPSQVAAAASCLSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLCFL--AFFACKVD-STGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGITALLLASKYEEMFSPN-----IEDFVYITDNAYTSSQIREMETLILKELKFELGRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LDGRDINGRMRAILVDWLVQVHSKFRLLQETLYMCIAIMDRFLQAQPVCRKK----LQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                             391
       FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 201; DB 1;
Pred. No. 5.9e-11;
4; Mismatches 134
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247DBAA412E6CBBD CRC64;
       (MPF).
                                                                                                                                                                                                                                                                                                                          328
                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
                                                                                                                            Gyoergyey J.,
       CYCLIN SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                      (CycMs2) (Fragment).
                                                                                                                                                                                                   core eudicots;
; Trifolieae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                Jonak C.,
                                                            AT THE
                                                                                                    cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                   Medicago.
                                                                                                                                                                                                               Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 7
CG2B_MM
ID CG2B_M
AC P46278
AC P46278
AC P46278
DT 01-NOV
DT 01-OCT
DE G2/m1t
OS Medican
OC Eukary
OC Sperma
OC Eukary
OC SPERMA
OC STRAIN
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RX MEDLIN
RX MEDLIN
RX MESKie
RA Heberl
RA Heberl
RA Heberl
RA Heberl
RA G0-to-
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Best Local
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                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae; Medicag
                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G2/mitotic-specific cyclin 2 (B-like cyclin) (CycMs2).
Meskiene I., Boegre L., Dahl M., Pirck M., Ha D.T.C.,
Heberle-Bors E., Ammerer G., Hirt H.;
"CycMs3, a novel B-type alfalfa cyclin gene, is induce
G0-to-G1 transition of the cell cycle.";
                                                               MEDLINE-95375541; PubMed-7647566;
                                                                                                                                                                                                      Medicago varia.
                                                                                                                                                                                                                                                                                         CG2B_MEDVA
P46278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000553; Cyclin.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                     NCBI_TaxID=36902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X68741; CAA48675.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB
                                                                                                                                                                                                                                                                                                                                                                                              274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 DIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFEYLS----RFQSRSLDANAREES--VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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TISSUE SPECIFICITY: ONLY EXPRESSED IN ORGANS WITH DIVIDING DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                            SEDQLLECSMLM
                                                                                                                                                                                                                                                                                                                                                                                                                           RKEKVIGCYQLM 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVSDL-THIADRAYTRKDILEMEKLMINTLQYNMSLPTAYVFMRRFLKAAQADKKLELVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDSC-----DANNSLAVVEYIEDLHAYYRKIEYLGCVSPTYMDEQLDUNERMRAILVD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S29925; S29925.
PQ0490; PQ0490.
P20248; 1JSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLISRATEIIVSNIQEASFLAYWPSCIAAAAILTA---ANEIPNWSVVKPENAESWCEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFF--A¢KVDSTGTFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK---LQLVGLVAMLIJACKYEEVSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LVDLSLVEYEMLKFPPSLVAAAAVYTAQCTVSGFKHWN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 AA;
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                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37710 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 200;
Pred. No. 5
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7E4CCB166B5D949E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                       434
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5.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                Swoboda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KTCEWHTNY
               'n
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SEQUENCE FROM N.A. STRAIN-CV. C24;

MEDLINE=92228771; PubMed~1373494; Hemerly A.S., Bergounioux C., van

van

Montagu

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RESULT 8
CG2B_ARATH
ID CG2B_A
AC P30183
DT 01-App
DT 16-OCT
DT 16-OCT
DE G2/mit
GN CYC1 0
OS Arabid
OC Eukary
OC Sperma
OC SPE
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Best Local :
                                                                                                                                                         CG2B_ARATH STANDARD; PRT; 428 AA.

P30183; Q42081;
01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
62/mitotic-specific cyclin (B-like cyclin).
CYCl OR AT4G37490 OR F6G17.140.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin; 1.

Pfam; PF02984; cyclin_C; 1.

SMART; SM00385; CYCLIN; 1.

PROSITE; PS00292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE C (MITOSIS) TRANSITION.

-i- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A SERINE/THREONINE KINASE HOLOEWZYME COMPLEX ALSO KNOWN AS MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

-i- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 WILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 DIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFEYLS----RFQSRSLDANAREES--VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFF--ACKVDSTGTFIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLISRATEIIVSNIQEASFLAYWPSCIAAAAILTA---ANEIPNWSVVKPENAESWCEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK----LQLVGLVAMLLACKYEEVSVP
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Pred. No. 8.3e-11;
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RA VOS P., Hohetsel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pottorya D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Granderath K., Dauner D.,
RA Bose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Glabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Ferol J., Torres A.,
RA Allons J., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Schnabl S., Hiller N., Goller P., Heber S., Francs P., Bielke C.,
RA Marer J., Fulton L., Mardis E., Dahte M., Babermann K.,
RA Schward J., Fulton B., Miller N., Greo T., Kemp K.,
RA Kamer J., Fulton L., Mardis E., Dahte M., Pepla K., Hillier L.,
RA Marer J., Berghoff A., Jones K., Donne K., Cotton M., Joshu C.,
RA Marer J., Berghoff A., Jones K., Donne K., Cotton M., Joshu C.,
RA Schull R., Berghof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genes regulating the plant cell cycle: isolation of a mitotic-like cyclin from Arabidopsis thaliana."; Proc. Natl. Acad. Sci. U.S.A. 89:3295-3299(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mayer K.F.X., Schueller C., Wambutt
Pohl T., Duesterhoeft A., Stiekema
                                                                                                                                           Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris B., Ansorge W., Brandt
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                          Submitted (SEP-1993)
                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 6-94 FROM N.A.
                                                                                                                                                                                                                                                                                                                 Philipps G.,
                                                                                                       ABRUPTLY DESTROYED AT MITOSIS.
SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 402:769-777(1999).
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    institutions as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ekema W., Entian K.-D., Te
P., Grivell L.A., Rieger
long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy G., Volckaert G.,
    its content
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CG22_YSAST
CG2_YSAST
CG22_YSAST
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Creat 01-MAR-1992 (Rel. 21, Last 15-JUL-1999 (Rel. 38, Last G2/mitotic-specific cyclin CLB2 OR YPR119W OR P9642.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; pF00134; cyclin; 1.
pfam; pF02984; cyclin_C; 1.
smarr; sm00385; cYCLIN; 2.
pROSITE; pS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A44123; A44123.
HSSP; P20248; 1JSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z26397; CAA81236.1;
                                                                                   "Cyclin-B
and in G2.
                    SEQUENCE FROM
                                                               Genes
                                                                                                          Richardson H., Lew 
"Cyclin-B homologs
                                                                                                                                                                              STRAIN-S288C
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                             Cell 65:145-161(1991)
                                                                                                                                                                                                                                                                    cerevisiae.
                                                                                                                                                                                                                                                                                                                 Nasmyth
                                                                                                                                                                                                                                                                                                                                      Surana U., Robitsch
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=91191554;
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P24869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG22_YEAST
                                                                                                                                                       MEDLINE=93051323; PubMed=1427070;
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                                                                                                                                                                                                                                                                                                                                   PubMed=1849457; ch H., Price C.,
                                                                                                            in
                                                                                                                                 D.J.,
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91 K -> N (IN REF. 1).
48459 MW; 83334927768D8857
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                                                                                                              Saccharomyces
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                                                                                                                                   Henze M.,
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Pred. No.
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                                                                                                                                 Sugimoto
                                                                                                              cerevisiae
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                                                                                                              Reed S.I.;
function in
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RESULT 10
CG21_SOYBN
ID CG21_SOYBN
AC P25011;
DT 01-MAR-1992
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R EMBL; X62319; CAA44195.1; -.

R EMBL; U40828; AAB68060.1; -.

R PIR; S14166; S14166.

R HSSP; P20248; 11SU.

R SGD; S0006323; CLB2.

R InterPro; IPR000553; Cyclin.

R Pfam; PF00134; cyclin; 1.

R Pfam; PF02984; cyclin_C; 1.

RR Pfam; PF02984; Cyclin_C; 1.

RR PROSITE; PS00292; CYCLIN; 2.

RR PROSITE; PS00292; CYCLIN; 1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE (MITOSIS) TRANSITION. INVERACTS WITH THE CDC2 PROTEIN KINASE FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT MITOSIS.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MINIMUM IN G1 PHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NDI--FEYLHQLEVITLPKKEDLYQHRNIHQN-RDILVNWLVKIHNKEGLLPETLYLAI
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                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 198.5; DB 1; 25.5%; Pred. No. 1.3e-10; tive 59; Mismatches 119;
                                                                           PRT;
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Best Local Similarity
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"ISOlation and characterization of cDNA clones for plant cyclins.";

"ISOlation and characterization of cDNA clones for plant cyclins.";

EMBO J. 10:2681-2688 (1991).

-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/

(MITOSIS) TRANSITION.

-i- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX ALSO KNOWN AS MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

-i- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABROPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00134; cyclin; 1.
PFAM; PF00294; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
Cyclin; Cell cycle; Cell division; Mitosis.
SEQUENCE 454 AA; 50094 MW; 54EB4596586A7C10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-CC7-2001 (Rel. 40, Last annotation update)
62/mitotic-specific cyclin S13-6 (B-like cyclin).
Glycine max (Soybean).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae
eurosids 1; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Glycine.
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                                                                                                                                                                                                142 PLVPSLLD-LQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGT
                                                                                                                                                                                                                                                                                                                                                                    26 PECSFSDIDSSPPPPSPTT----EDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANARE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                        VVKPENAESWCEGLRKEKVIGCYQLM
                                                                              -VRFIKASVPDQELDNM--AHFLSELGMMNYATLMYCPSMVAASAVLAARCTLNKAPFWN
                                                                                                                    FIRFLISRATEIIVSNIQEASFLA-----YWPSCIAAAAILTA---ANEIPNWS
                                                                                                                                                                                                                                                                    ESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEE
                                                                                                                                                                                                                                                                                                                           PKEQIIDIDASDVDNELAAVEYIDDIYKFYKLVENESR---PHDYIG--SQPEINERMRA
ETLKLHT - - -
                                                                                                                                                            ILVDWLIDVHTKFELSLETLYLTINIIDRFLAVKTVPRRE----LQLVGISAMLMASKYEE
                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 197.5; DB 1
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYCLE AT THE G2/M
                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                           227
                                                                                387
                                                                                                                      246
                                                                                                                                                                                                                                             284
                                                                                                                                                                                                                                                                                                                                                                                                            11;
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RESULT 11 CG2A\_DAUCA ID CG2A\_D AC P25010

CG2A\_DAUCA P25010;

STANDARD;

PRT;

341 A

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RESULT 12
CG2B_ORYSA
ID CG2B_O
AC Q40671
DT 15-DEC
DT 15-DEC
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                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
 CG2B_ORYSA
Q40671;
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last anotation update)
G2/mitotic-specific cyclin Cl3-1 (A-like cyclin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and characterization of cDNA clones for plant cyclins."; EMBO J. 10:2681-2688(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daucus carota (Carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X62819; CAA44631.1; -. PIR; S16521; S16521. HSSP; P20248; LJSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hata S., Kouchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91330894; PubMed=1831125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000553; Cyclin
                                                                                                                                         254
                                                                                                                                                                                                                                                                             144 VNVL---NRQKLQLLGVSSFLIASKYEEIKPKNVADF-VDITDNTYSQQEVVKMEADLLK
                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ARE ABRUPTLY DESTROYED AT MITOSIS.
SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                         SLIAASVTFLARFTIRPNVNPWSI----ALQKCSGYKSKDLKECVLLLHDL
                                                                                                                                                                          SCIAAAAILTAANEI-PN---WSVVKPENAESWCEGLRKEKVIGCYQLMQEL
                                                                                                                                                                                                                                            VLDWRLRSVTPLCFLAFF-ACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYW-----P
                                                                                                                                                                                                                                                                                                            SRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLG
                                                                                                                                                                                                                                                                                                                                                                             IEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLD
                                                                                                                                                                                                                                                                                                                                                                                                              DLLCRE-----FEVPKCVAQKKRKRGVKEDVGVDFGEKFDDPQMCSAYVSDVYEYLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               DLLCGEDSSGILSGESPEC-------SFSDIDSSPPPPSPTTEDCYSIASF
                                                                                                                                                                                                                                                                                                                                               MEMETKRRPMMNYIEQVQ-KDVTSNMRGVLVDWLVEVSLEYKLLPETLYLAISYVDRYLS 143
                                                                                                                                                                                                       TLKFEMGSPTVKTFLGFIRAVQENPDVPKLKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Similarity | 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KURODAGOSUN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 AA;
   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                     STANDARD

    Created)
    Last sequence update)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuka I., Ishii T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.5; DB Pred. No. 1.3e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5708DF4269C06F3F CRC64;
                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                     419
                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                           -EFLANYLAELSLLDYGCLEFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                            275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                              173
                                                                                                                                                                                                                                                                                                                                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                                 84
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the CycB2 type from rice.";
(In) Plant Gene Register PGR97-001.
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE (MITOSIS) TRANSITION.
-1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX ALSO KNOWN AS MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95261415; PubMed=7742859; Sauter M., Mekhedov S.L., Kende H.; Sauter M., Mekhedov S.L., Kende H.; "Gibberellin promotes histone HI kinase activity and the expression of cdc2 and cyclin genes during the induction of rapid growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last annotation update)
G2/mitotic-specific cyclin 2 (B-like cyclin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deepwater rice internodes."; Plant J. 7:623-632(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
SEQUENCE 419 AA; 47572 MW; A8774B56BD839A5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sauter M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X82036; CAA57556.1;
HSSP; P20248; 1FIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
                               251
                                                                                                                                                                                                                                                                               133
                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
ENAESW---CE---GLRKEKVIGCYQLMQEL
                                                                                                                                                                                                                                                                               LSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFF-
                                                                                                                                                                                                                                                                                                                                              NDINEKMRGILIDWLIEVHYKLELLDETLFLTVNIIDRFLARENVVRKK----LQLVGVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMGSELKEIEMEDIEEAAPDIDSCDANNSLAVVEYVDEIYSFYRRSEGLSCVSPNYMLSQ 187
                                                                                                                                                                                                                      MLLACKYEEVSVPVVEDL-ILICDRAYTRTDILEMERMIVNTLQFDMSVPTPYCFMRRFL
                                                                                                                                                                                                                                                                                                                                                                                                       RSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILSGESPECSFSDIDSSPPP-PSPTTEDCYSIASFIEHERNFVPGFEYLS-----RFQS
                                                                                           KAAQSDKKLELMSFF---
                                                                                                                                                       -ACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIN GAEW 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIN GAEW 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%;
                                                                                           -IIELSLVEYEMLKFQPSMLAAAAIYTAQCTINGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 196.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Cyc0s2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                 244
                                                                                                                                                                                                                                                                                                                                                                                                             132
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                                                                                                 352
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353

---KSWNKCCELHTKYSEEQLMECSKMMVEL 380

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á
                                                     Matches
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    EMBL; M65069; AAA34501.1; EMBL; M62389; AAA35019.1; EMBL; Z72893; CAA97112.1; PIR; A23700; A23700. PIR; S14165; S14165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG21_YEAST
P24868;
01-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                          Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; Multigene Cyclin; Cell cycle; Cell division; Mitosis; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wedler H., Scharfe M., Wedler E., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M

-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M

-I- FUNCTION: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ghiara J.B., Richardson H.E., Sugimoto K., Wittenberg C., Reed S.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-91191554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Surana U.,
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15-JUL-1999 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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S0003340; CLB1
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  ECSFSDIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANA---
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21, Last sequal 38, Last annotation
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                                                42;
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Pred. No. 1.
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RESULT 14
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15-JUL-1999
16-OCT-2001
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                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                     -I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M (MITOSIS) TRANSITION.
-I- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-I- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                     "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
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Mammalia; Eutheria;
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Eukaryota; Metazoa; C
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Submitted (DEC-1998) to
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(MAY-1997)
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(Rel. 38, Last sequence up
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specific cyclin B2.
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Primates;
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EMBL/GenBank/DDBJ databases
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                                                            Usage
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Matches 83
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Cyclin; C
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Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
                                                                                            MEDITINE-94148008; PubMed-8313906;
MEDITINE-94148008; PubMed-8313906;
MEDITINE-94148008; PubMed-8313906;
Pobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
Pobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
Pobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
Patterns of cell division revealed by transcriptional regulation of genes during the cell cycle in plants.";

EMBO J. 13:616-624(1994).

1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
(MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
AND ARE ABRUPTLY DESTROYED AT MITOSIS.

1- SUBBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX.

1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P34800;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G2/mitotic-specific cyclin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Antirrhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4151;
                                                                                                                                                                                                                                                                                                                                                                                                    Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 --KLPLLKVLPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LCGEDSSGILSGESPECSFSDIDS----SPPPPSPTTEDCYSIASFIEHERNEVPGFEYL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                          ABRUPTLY DESTROYED AT MITOSIS. SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSQKVLGQGKWNL-----KQQYYTGYTENEVLEVMQHMAKNVVKVNENLTKFIAIKNKYA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPLPLHFLRRASKAGEVDVEQHTLAKYLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYI----FEPRTIRRMELLVLGVLDWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LDGRDINGRMRAILVDWLVQVHSKFRLLQETLYMCVGIMDRELQVQPVSRK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCQAFSDALL-----CKIEDIDNEDWENPQLCSDYVKDIYQYLRQLEVLQSINPHF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLQLVGITALLLASKYEEMFSPN-----IEDFVYITDNAYTSSQIREMETLILKELKFEL
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AL080146; CAB45739.1;
P20248; JJSU.
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SM00385; CYCLINS: 1.
; PS00292; CYCLINS: 1.
Cell cycle; Cell division; Mitosis.
Cell cycle; Cell division; Mitosis.
45281 MW; 874466E1DD68A4C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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26.5%;
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Pred. No. 1.7e-10;
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Best Local
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HSSP; P30274; 1VIN.
InterPro; IPR000553; Cyclin.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X76122; CAA53728.1; -.
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                                                                                                                                                                                                        196
363
                                                                  307
                                                                                                                                    251
                                                                                                                                                                  105 VNYMDRFLDSRRLPETNGWPLQLYSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTI 164
                                                                                                                                                                                                                                        45 EDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLA 104
                                                                                                                                                                                                        EDMYKFYKSVENESR---PHDYMG--SQPEINEKMRAILIDWLVQVHHKFELSPETLYLT
                              YWPSCIAAAAILTA---ANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLM 272
                                                                  LVMEKKILGALEWYLTVPTPYVFLVRF-IKASMTDSDVENMVYFLAELGMMNY---ATLI
                                                                                                                                    INTVDRYLASE---TTTRRELQLVGIGAMLIASKYEETWAPEVHEL-VCISDNTYSDKQI
YCPSMIAAASVYAARCTLNKAPFWNETLQLHT----
                                                                                                RRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLA
                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                              11.1%; Score 194.5; 26.8%; Pred. No. 3e-
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-GFSEPQLMDCAKLL
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                                                                                                                                                                                                                                                                                                                 Length 473;
                                                                                                                                                                                                                                                                                 Indels
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Search completed: October 23, 2002, 14:38:29
Job time: 15 secs

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Result
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length: 2000000000
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Match
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1758
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sp_rodent:*
sp_virus:*
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sp_unclassified:*
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 330
372
354
368
373
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343
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367
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361
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361
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                                                                                                                                                DB
  90
Q9ZRX9
Q9SXW1
Q9SXW1
Q9SNV1
Q9FKP7
Q9FGQ7
Q9FGQ7
Q9FRD1
Q9SMD4
Q9SMD5
Q9SMD5
Q9SMD5
Q9SMD5
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                                                                                                                       Q9SNV2
P93103
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1954.843 Million cell updates/sec
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09fkp7
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09sn11
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P93103
09zrx9
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 Q91x96
Q40338
1 antirrhinum
7 arabidopsis
7 arabidopsis
7 arabidopsis
1 arabidopsis
4 lycopersico
5 lycopersico
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8 medicago sa
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3 chenopodium
9 nicotiana t
7 nicotiana t
8 nicotiana t
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## ALIGNMENTS

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RESULT
Q9SNV2
                                   Query Match
Best Local S
Matches 192
                                 Q9SNV2;
Q9SNV2;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
                                                                                                                                SEQUENCE FROM N.A.
Gaudin V., Lunness P., Fobert P., Towers M., AACU .......
Murray J., Coen E., Doonan J.H.;
"The expression of D-cyclin genes define distinct developmental
The expression of D-cyclin genes and is locally regulated by the
                                                                                                                                                                                                    Antirrhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
                                                                                                                                                                                                                                          CYCD1
                                                                                                                                                                                                                                                 CYCLIN D1.
                                                                                                                                                                                            NCBI_TaxID=4151;
192;
          Similarity
                                                                                                                                                                                                                                                        0 (TrEMBLrel.
0 (TrEMBLrel.
1 (TrEMBLrel.
 Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
         51.6%; Score 907.5; DB 56.1%; Pred. No. 3.6e-83
                                                                                                                                                                                                                                                         13,
13,
52;
                                                                                                                                                                                                                                                         Last sequence up
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 Mismatches
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                 DB 10;
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 77;
Indels
                  Length
21;
Gaps
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MSVSCLSDY-DLLCGEDSSGILSG---ESPECSFSDIDSSPPPPSPTTEDCYSIASFIEH 56

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PRESULT PRESULT IN PRE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
RCBI_TaxID=3560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYCLIN-D LIKE PROTEIN. CYCL1.
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01-MAY-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1. SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE EMBL; Y10162; CAA71244.1; -. InterPro; IPR004366; Cyclin. InterPro; IPR004367; Cyclin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Nucleotide sequence of a cDNA encoding a D-type cyclin photoautotrophic cell suspension culture of Chenopodium Plant Physiol. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00292; CYCLINS; 1.
Cell cycle; Cell division; Cyclin
SEQUENCE 372 AA; 41768 MW; 6D
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DWIHKVQSHYNFGPLCVYLSVNYLDRFLSAYELP-GKAWMMQLLGVACLSLAAKVDETDV
                                                                                                                                                                                  ILLIIIKEHNFEALISGFFVANHECLASLFDNERQHFLGLDYLKRFRNGDLDLGARNLVI
                                                                                                                 GWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLV 144
                                                                                                                                                                                                                                                                                                                           YDLLCGEDSSGILSGESPECSFSDIDSSPPPPSPTTEDCYSI --
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       Score 463.5;
Pred. No. 2.8e
66; Mismatches
                                                                                                                                                                                                                                ----ASFIEHERNFVPGFEYLSRFQSRSLDANAREESV
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PLANT 19892; CAAO9852.1; -.

REMBL; AJO11892; CAAO9852.1; -.

REMBL; AJO11892; CAAO9852.1; -.

RINTERPOO; IPRO04366; CYCLIN_C.

PEAM; PF00134; CYCLIN_C.

RINTERPOO; IPRO04367; CYCLIN_C.

PEAM; PF00134; CYCLIN_C.

REMBL; PF00134; CYCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, I
01-DEC-2001 (TrEMBLrel. 19, I
CYCLIN D2.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).

Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99097070; PubMed=9880377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348
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                                                                                                                                                                                                                                                                                       WTVQLLAVACLSLAAKMEEINVPLTVDLQVGDPKFVFEGKTIQRMELLVLSTLKWRMQAY
                                                                                                                                                                                                                                                                                                               WPLQLYSVACLSLAAKMEEPLYPSLLDLQIEGAKYIFEPRTIRRMELLYLGYLDWRLRSV
                                                                                                                                                                                                                                                                                                                                                                                    KDDYVERLRSGDLDLSVRKEALDWILKAHMHYGFGELSFCLSINYLDRFLSLYELPRSKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFDDVDSLTISQQN--IETKSKDLSFNNGIRSEPLIDLPSLSEECLSF--MVQREMEFLP
CLSYKSGDERTVGSCTTSSHT----
                                                                                          QAKDIDKA--MPCFFIHLDKGRVQKCVELIQDLT-TATITTAAAASLVPQSPIGVLEAAA
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                                                                                                                                           PNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQ-----LRVTT
                                                                                                                                                                                            TPYTFIDYFMRKMNGDQIPSRPLISGSMQLILSIIRSIDFLEFRSSEIAASVAMSVSGEI
                                            RTRMRSS---TVSSFSSSSTSFSLSCKRKLN
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Last annotation update)
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PRESULT 4

QUESTO 101-M

POT 01-M

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RESULT 5
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ID Q92RR
AC Q92RR
AC Q92RR
AC Q92RR
DT 01-M
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-i- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

R EMBL; AB015222; BAA76478.1; -.

R InterPro; IPR004366; Cyclin.

R InterPro; IPR004367; Cyclin_C.

R InterPro; IPR004367; Cyclin_C.

R Pfam; PF00134; cyclin; 1.

R Pfam; PF00384; cyclin; 1.

R SMART; SM00385; CYCLIN; 1.

R SMART; SM00385; CYCLINS; UNKNOWN_1.

Gell cycle; Cell division; Cyclin.

Gell cycle; Cell division; Cyclin.
                                                                                                        O9ZRX8

PRELIMINARY; PRT; 373 AA.

C Q9ZRX8;

T 01-MAY-1999 (TrEMBLrel. 10, Created)

T 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

CYCLIN D3.1 PROTEIN.

CYCL3.1.

CYCL3.1.

S Nicotlana tabacum (Common tobacco).

S Nicotlana tabacum (Common tobacco).

S Nicotlana tabacum (Streptophyta; Embryophyta; Trace Spermatophyta; Magnoliophyta; eudicotyledons; core eudic Spermatophyta; euasterids I; Solanales; Solanaceae; Nicotlana constraints.
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Q9SXN7;
Q1-MAY-2000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

MCBI_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTCYCD3-1 PROTEIN. NTCYCD3-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sekine
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    SEQUENCE FROM N.A
                                                                              NCBI_TaxID-4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRKEAVKWILKVNAHYGESTETAILAINYEDRELSSLHEQKDKPWMIQLVÄVTCLSLAAK 146
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                                                                                                                                                                a; Tracheophyta;
eudicots;
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RESULT
Q9SNV1
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Best Local
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Q9SNV1;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
NCBI_TaxID=4151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 373 AA; CYCLIN; 1.

PROSITE; PS00292; CYCLIN; UNKNOWN_1.

PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.

Cell cycle; Cell division; Cyclin.

SEQUENCE 373 AA; 42980 MW; 597F0994ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C;
SMART; SM00385; CYCLIN; 1
                                                                                                                                                   in Antirhinum apical meristems and is locally cycloidea gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ-1-SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
EMBL; AJ250397; CAB61222.1;
InterPro; IPR004367; Cyclin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYCLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                       Cell cycle;
                                                             Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin; 1.
SMARP; SM03385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                              Gaudin V., Lunness P., Fobert P., Towers Murray J., Coen E., Doonan J.H.;
"The expression of D-cyclin genes define
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYCD3A
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y-2000 (TremBlrel. 1)
Y-2000 (TremBlrel. 1)
C-2001 (TremBlrel. 1)
N D3A (FRAGMENT).
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IPR004367; Cyclin_C.
IPR002114; PTS_HPr_ser.
  343 AA;
                       Cell division; Cyclin. 343 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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13,
19,
  MW.
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Last sequence update)
Last annotation update)
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Pred. No. 2.2e-34;
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  128210AB2FC6E2C6 CRC64;
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RESULT 7
Q9FKP
ID Q9FKP
AC Q9FKP
AC Q9FK
AC Q01-1
DT 01-1
DT 0
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Best Local :
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
D-TYPE CYCLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
EMBL; AB011479; BAB11564.1; -.
EMBL; BR011479; BAB1564.1; -.
InterPro; IPR004365; Cyclin.
SMART: SM00385; CYCLIN; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SÉQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00292; CYCLINS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98344145; PubMed-9679202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGW 123
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                             PETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDW
                                                                                                                                                          NEVPGEEYLSREQSRSLDAN-AREESVGWILKVHAYYGFQPLTAYLAVNYMDRELDSRRL 117
                                                                                                                                                                                                                            ELSLLCTESNVDDEGMIVDETPIEISIPQMGFSQSESEE----
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                                                                                                                                                                                                                                                                                                                                                         53;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   Score 420.5;
Pred. No. 4.8
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01-MAR-2001 (TIEMBLIEL 16, Last sequence up
01-DEC-2001 (TIEMBLIEL 19, Last annotation
CYCLIN D3-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
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                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, D-TYPE CYCLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Katoh T.,
Tabata S.;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                            Q9XFR7
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                                     CYCD4.1.
                                                                                                                        Q9XFR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 PSGKGWILQLLAVACLSLAAKIEETEVPMLIDLQVGDPQFVFEAKSVQRMELLVLNKLKW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AAILTAANEI-------PNWSVVKPENAESWCEGLRKEKVIGCYQ 270
                                                                                                                                                                                                                                 303 DQDSPSGYLDFDDSSNSSWNYSTTASVSSSSSPEPL-LKRRRVQEQQMRLPSINRMFLD
                                                                                                                                                                                                                                                                  291 PQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 EHERNFYPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 23.9%; Score 419.5; DB 10; Length 367; Local Similarity 35.7%; Pred. No. 7.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLRAITPCSYIRYFLRKMSKCDQEPSNT----LISRSLQVIASTTKGIDFLEFRPSEVAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLRSVTPLCFLAFF-----ACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAIMILVFEELKPCDEVEYQSQITTLLKVNQEKVNECY----ELLLEHNPSKKRMMNLV
                                                                                                                                                                                                                                                                                                                        AAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLPLLKVL
                                                                                                                                                                                                                                                                                                                                                                     LQWRMHPVTPISFFDHIIRRFGSKWHQQLDFCR----KCERLLISVIADTRFMRYFPSVL
                                                                                                                                                                                                                                                                                                                                                                                                    LDWRLRSVTPLCF----LAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENETHPCFGEQILDGFL-----VSCRKEALDWVLRVKSHYGFTSLTAILAVNYFDRFMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 AA;
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                                                                                                                                            PRELIMINARY;
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"A new D-type cyclin of Arabidopsis thaliana expressed croot primordia formation.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
EMBL; AJ131635; CAB41347.1;
InterPro; IPR004366; Cyclin.
InterPro; IPR004366; Cyclin.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSNII PRELIMINARY; PRT; 361 AA.
OSSNII;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN D3-LIKE PROTEIN (AT3G50070/F3A4_150).
F3A4.150.
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SMART; SM0385; CYCLIN; 1.

PROSITE; PS00292; CYCLINS; UNKNOWN_1.

Cell cycle; Cell division; Cyclin.

SEQUENCE 308 AA; 34687 MW; 591ADA3361DDD63D CRC64;
                                                                                                                                                                                                                               Bargues
Mewes H.
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de Veylder L., De Almeida
                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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  Bowser L.,
                                                    SEQUENCE FROM N.A.
                                                                                                         Submitted
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bmitted (DEC-1999)
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                                                                                                                                                                                                     ., Collado M.C., Navarro P., Terol J., Perez-Alonso ., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat ! (NOV-1999) to the EMBL/GenBank/DDBJ databases
                               Chen
     Carninci
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-1999) to the EMBL/GenBank/DDBJ
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Pred. No. 1.2e-33;
  Koesema E., Meyers
J.M., Goldsmith A.
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                            J.,
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Matches 109
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                                                                                                                                                                                                                                                                                                                                                     O9SMD4
Q9SMD4;
Q1SMD4;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-DEC-2001 (TrEMBLrel. 19,
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  Kvarnheden A., Yao J.L., Zhan X., (
"Isolation of three distinct CycD3 development in tomato.";
J. Exp. Bot. 51:1789-1797(2000).
                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. UC82B;
MEDLINE-2056011; PubMed-11113158;
                                                                                                                                                                                                             Lycopersicon esculentum (Tomato).

Embryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                  CYCD3,3
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Submitted (AUG-2001) to the
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                                                                                                                                                                                                                                                                                                                                      CYCD3, 3 PROTEIN
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                                                                                                                                                                                         NCBI_TaxID=4081;
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Pred. No. 5.4e-33;
59; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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RESULT 12
Q9SMD5
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Best Local Similarity
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SMD5;
Q1-MAY-2000 (TrEMBLrel. 13, C:
Q1-MAY-2000 (TrEMBLrel. 13, L:
Q1-DEC-2001 (TrEMBLrel. 19, L:
CYCG3,2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. UC82B;
STRAIN-CV. UC82B;
MEDLINE-20566012; PubMed-11113158;
MEDLINE-20566012; PubMed-11113158;
MEDLINE-20566012; PubMed-11113158;
MEDLINE-20566012; PubMed-11113158;
                                                                                                                                      Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1 SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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InterPro; IPR004367; Cyclin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY:
EMBL; AJ002590;
                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY EMBL; AJ002589; CAB60837.1; -.
                                                                                                                                                                                                                                                                                                                                        development in tomato.";
J. Exp. Bot. 51:1789-1797(2000)
                                                                                                                                                                                                                                                                                                                                                                                              Kvarnheden A., Yao J.L., Zhan X., O'Brien I., Morr
"Isolation of three distinct CycD3 genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYCD3,2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                     PROSITE; PS00292; CYCLINS; UNKNOWN_1.
Cell cycle; Cell division; Cyclin.
SEQUENCE 364 AA; 41791 MW; A5F965
                                                                                                                                                                                                                          InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9SMD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 TGVMDMSFSSDYSNDSWSVATSVTSSPEPLSKKIRESN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
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PRO2984; cyclin,C: 1.

Fr. SM00385; CYCLIN: 1.

Cycle; Cell division; Cyclin.

ENCE 336 AA; 38687 MW; 5BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSVVKPENAESWCE-----GLRKEKVIGCYQLMQELVIN----NNQRKLPLLKVLPQLR 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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22.8%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 2.8e-
Score 401;
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                                                        A5F9657DEFEF4CA5 CRC64;
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DB 10;
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Length 364;
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RESULT 13
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
-- ~~~ (TrEMBLrel. 19,
                                                                                                                                                                                                                                        PROSITE; PS00292; CYCLINS; UNKNOWN_1.
Cell cycle; Cell division; Cyclin.
SEQUENCE 359 AA; 40971 MW; 8CDAF8
                                                                                                                                                                                                                                                                                          Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1. SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. EMBL; AJ002588; CAB60836.1; -. EMBL; AJ245415; CAB51788.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Joubes J., Walsh D., Raymond P., Chevalier C.; "Molecular characterization of the expression of distinct classes cyclin during early development of tomato fruit."; submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. CV WEST VIRGINIA 106; TISSUE-YOUNG FRUIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Note and development"; No., O'Brien I., Morris B.;
"Differential expression of three D3 cyclin genes during tomato set and development";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; euasterids I; Solanales; Solanaceae; Solanum.
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InterPro; IPR004367; Cyclin_C.
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117 LPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLD 176
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                                                                                                  13 ISALLD-GLYCEEDR--FLDDDLGEWSSLDVGNENVKKTLPLLECDMFWEHDELATLLSK 69
                                                                                                                                     3 VSCLSDYDLLCGEDSSGILSGESPECSFSDIDSSPPPPSPTTEDC-----YSIASFIEH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQEL---VINNNQRK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOKDKPWMTQLAAVTCLSLAAKVEETQVPLLLDFQVEDAKYVFEAKTIQRMELLVLSSLK 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRMNPVTPLSFLDHIIRRLGLKNNVHWEFLRRCESLLLSVMIDCRFVRYMPSVLATAIML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPETNGWPLQLYSVACLSLAAKMEEPLYPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLD 176
                                                                  ERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRR 116
                                  ENEFHLGFQ--SLISDGSL-MGARKEALDWMLRVIAYYGFTATTAVLAVNYFDRFVSGWC 126
                                                                                                                                                                       115;
                                                                                                                                                                                       Similarity
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                       21.8%; Score 383; DB 10; 32.7%; Pred. No. 3.6e-30;
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9; Mismatches 92;
                                                                                                                                                                                                                                           8CDAF848272484A0 CRC64;
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chevalier C.;
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082136;
01-NOV-1998
01-NOV-1998
01-DEC-2001
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Pfam; PF02984; cyclin_C; 1.

SMART; SM00385; CYCLIN; 1.

PROSITE; PS00292; CYCLINS; UNKNOWN_1.

Cell cycle; Cell division; Cyclin.

SEQUENCE 384 AA; 43859 MW; 34BCO9;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I, Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Analysis of cycles of dormancy and growth in pea axillary on mRNA accumulation patterns of cell cycle-related genes." Plant Cell Physiol. 39:255-262(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimizu S., Mori H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-98249622;
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GVIDAVFSSDGSNDSWKVGSSSYSTS
                                            STVSSFSSS-----SSTSFSLS 320
                                                                                                                                                                                                                                                                                                                        EEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVD-ST
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                                                                                                                                             VVKPENAESWCEGLRKEKVIGCYQLMQELVINNN---QRKLPLLKVLPQLRVTTRTRMRS
                                                                                                                                                                                                                                              GTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPN---
                                                                                                                                                                                                                                                                                              EETQVPLLLDLQVQDTKYVFEAKTIQRMELLILSTLKWKMHPVTPHSFLDHIITRLGLKT
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                                                                                                                                                                                            RCENLLLSVLLDSRFVGCVPSVLATATMLHVIDQIEESDDNGVDYKNQLLS
                                                                                           ---INKEKVDECYNAIVEVTNENNYGHKRKYEQIPGSP--
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Last sequence update)
Last annotation update)
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RESULT 15
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AC Q9LX9
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Q9LX96;
Q9LX96;
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-DCC-2001 (TrEMBLrel. 19, L
CYCLIN PROTEIN-LIKE.
F12B17_210.
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SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; UI
SEQUENCE 317 AA; 35910 MW
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL353995; CABB9399.1; -.
InterPro; IPR004366; Cyclin.
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Bevan M., Bancroft I.,
Submitted (APR-2000) to
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273 G---EMIERDGSSSSSQTPNNTVL----QFKSRRYSHSLSTASVSSSLTSLS 317
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                                                               GCYQLMQELVINNNQRKLPLLKVLPQLRVTTRTRMRSSTVSSFS-SSSSTSFS 318
                                                                                                                               GVLIVDVWAGIDFLEFRASEIAAAVALSVSGEHFDKFSF----SSSFSSLEKERVKKI
                                                                                                                                                                    -----EASFLAYWDSCIAAAAILTAANE-IPNWSVVKPENAESWCEGLRKEKV--I
                                                                                                                                                                                                                                                                                                                    LVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRF-LISRATEIIVSNIQ------
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the EMBL/GenBank/DDBJ databases
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WW; 07616F8480927711 CRC64;
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Search completed: October 23, 2002, 14:39:07 Job time: 32 secs

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Result
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seq length: 2000000000
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Copyright (c) 1993 - 2002 Compugen
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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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US-08-522-166-8
US-08-480-312-8
US-08-480-312-8
US-08-464-517-19
US-08-463-772-15
US-08-464-517-4
US-08-464-517-4
US-08-463-772-4
US-08-246-361A-4
PCT-US93-05000-4
US-08-770-761A-7
US-08-770-761A-7
US-08-460-694-2
US-08-770-761A-3
US-08-770-761A-3
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US-08-522-166-8
                                                                       ; ORGANISM: US-08-522-166-8
              Query Match
Best Local Similarity
Matches 75; Conserv
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STREET: 2800 Pa
CITY: Seattle
STATE: Washingi
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                Conservative
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## ALIGNMENTS

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Sequence 8, Application US/08522166
Patent No. 5783661
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORD OF WINDOWS 3.1
SOFTWARE: WORD FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NEWSON
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FILING DATE: June 7, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,309
APPLICATION NUMBER: 07/764,309
                                                                                                                       MOLECULE TYPE: protein
DESCRIPTION: Cyclin B polypeptide sequence; Figure
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: September 20, ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, TITLE OF INVENTION: Human Cyclin E NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
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2800 Pacific First Center, 1420 Fifth Avenue
                                                                                           Homo Sapiens
                 10.3%;
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ber 20, 1991
31;
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               Score 180.5; DB 1
Pred. No. 3.3e-12;
Mismatches
                                   DB 1;
101;
Indels
                                   Length
                                     432;
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49;
Gaps
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                 MOLECULE TYPE: protein
DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,309
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 DMSIVLEDEKP----VSVNENP----DYHEDIHTYLR--EMEVKCKPKVGYMKK--QPDI 206
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                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
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16 DSSGILSGESPECSFSDIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSL 75
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                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sheiness, Diana K. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/488,382A FILING DATE: June 7, 1995
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                                               Conservative
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                                                                                                                                                     Homo Sapiens
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                                         10.3%; Score 180.5; DE 29.3%; Pred. No. 3.3e-1 tive 31; Mismatches 1
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US-08-480-912-8
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                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                MOLECULE TYPE: protein
DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
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159 DMSIVLEDEKP----VSVNENP----DYHEDIHTYLR--EMEVKCKPKVGYMKK--QPDI 206
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                                          16 DSSGILSGESPECSFSDIDSSPPPPSPTTEDCYSIASFIEHERNFVPGFEYLSRFQSRSL 75
                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-Windows 3. SOFTWARE: Word for Windows-6.0
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CITY: Seattle
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                                                                                      Local Similarity
les 75; Conserv
                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sheiness, Diana K REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TGQSWPESL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101-2347
                                                                                                                                                                                                                                                                                                                    : 432 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F. VENTION: Immunoassays for Detection of Human Cyclin E
                                                                                                                                                                                                                                                                                                                                                                                                           1-206-224-0779
                                                                                    Conservative
                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                            Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           September 20, 1991
                                                                                                                                                                                                                                                                                                   single
                                                                                                        10.3%; Score 180.5; DB 2; 29.3%; Pred. No. 3.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07/764,309
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                                                                                  Mismatches
                                                                                      101;
                                                                                                                            Length 432;
                                                                                      Indels
                                                                                      49;
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                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-464-517-19
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                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY,AGENT INFORMATION:
NAME: MATTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
                                                                                                                                                                                                                                                                TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: BEACH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 WSVVKPENAESWCEGL 260
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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LRAMLKAEETCAPSVSYFKCVQKEVL-PSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLD 86
                              IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASKFEEIYPPEVAEF-----VYITDDTYTKKQVLRMEHLVLKVLTFDLAAPTVNQFLTQY 318
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                                                                     10.18; ilarity 25.28; Conservative 45
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                                                                        45;
                                                                     Score 177.5; DB 2;
Pred. No. 4e-12;
5; Mismatches 108;
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                                                                   108;
                                                                                                 Length 295;
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                                                                 Gaps
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LRAMLKAEETCAPSVSYFKCVQKEVL-PSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLD 86
RFLDSRRLPETNGWPLQLVSVACLSLAAKMEE--PLVPSLLDLQIEGAKYIFEPRTIRRM 167

RFLSLEPVKKSR---LQLLGATCMFVASKMKETIPLTAEKLCIYTDGS---IRPEELLQM 140

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US-08-246-361A-19
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       Matches
                      Best Local Similarity
                                           Query Match
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                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 295 amino acid
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227 7400
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                            FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,36
FILING DATE: 19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES
NUMBER OF SEQUENCES: 50
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APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 SMVAAGSVVAA---VKGLNLRSPNNFLSYYRLTRFLSRVIKC 239
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                                                                                                                               STRANDEDNESS:
                                                                                                                                                     TYPE:
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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5998582
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                                                                                                                                                                  295 amino acids
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       Conservative
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                                                                                                                  linear
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                  10.1%; Score 177.5; DB 2; 25.2%; Pred. No. 4e-12;
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   45; Mismatches
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     108;
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 Indels 13;
                                   Length
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Gaps
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US-08-463-772-19; Sequence 19, Ap; Patent No. 6066
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Best Local :
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APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEACH, I
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 295 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1
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141 ELLLVNKLKWNLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPP 200
                                                                                                        110 RFLDSRRLPETNGWPLQLVSVACLSLAAKMEE - PLVPSLLDLQIEGAKYIFEPRTIRRM 167
                                  168 ELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                      87 RFLSLEPVKKSR----LQLLGATCMFVASKMKETIPLTAEKLCIYTDGS----IRPEELLQM 140
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                              28 LRAMLKAEETCAPSVSYFKCVQKEVL-PSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLD 86
                                                                                                                                                                                  50 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWP 227
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25.2%;
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                                                                                                                                                                                                                                       Score 177.5; DB 3; Pred. No. 4e-12;
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PCT-US93-05000-2
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            Sequence 19, Application PC/TUS9305000 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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APPLICATION NUMBER: US/0
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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APPLICANT:
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                                                                                                                                                 SCIAAAAILTAANEIPNWSVVKPENAESWCEGLR-KEKVIGC 268
                                                                                                                                                                                                                   ELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWP
                                                                                                                                                                                                                                                                                   RFLDSRRLPETNGWPLQLVSVACLSLAAKMEE--PLVPSLLDLQIEGAKYIFEPRTIRRM 167
                                                                                                                                                                                  ELLLVNKLKWNLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPP
                                                                                                                                                                                                                                                     RFLSLEPVKKSR---LQLLGATCMFVASKMKETIPLTAEKLCIYTDGS---IRPEELLQM
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56; Conserv
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AMINO ACID
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25.2%;
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Pred. No. 4e-12;
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US-08-464-517-4
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Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: AMINO ACID
                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
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CORRESPONDENCE ADDRESS:
                                                                                                                                NUMBER OF SEQUENCES: 50
CORRESDONTENOT .... 50
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PRIOR APPLICATION DATA:
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 COMPUTER READABLE FORM:
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         COUNTRY: US.
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STREET: 0.
TMY: Boston
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US-08-463-772-4
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Patent No. 6066501
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APPLICANT: BEACH, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 --- IKPQELLEWELVVLGKLKWNLAAVTPHDFIEHILRKLPQQREKLSLIRKHAQTFIAL
                                                                                                                                                                                                                                                                                                                                                                              274 ELVINNORKLPLLKVLPQLRVTTRTRMRS 303
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                                   COUNTRY: UZIP: 02109
                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                         STATE:
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                                                                                                                          ADDRESSEE:
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IBM PC compatible
                                                                                                                            LAHIVE & COCKFIELD
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UMBER: US 07/888,178
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                                                                                                                                                            D-TYPE CYCLIN AND USES RELATED THERETO: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227-7400
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Indels 19; Length 309;

Gaps

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US-08-246-361A-4
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                                                                                                                                                                                      Sequence 4, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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APPLICATION NUMBER: US 07/988,178
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                     268 D-----QIEAVLINSLQQYRQDQRDGSKS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 ELVINNNORKLPLLKVLPQLRVTTRTRMRS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CATDFKFAMYPPSMIATGSVGAAICGLQQDEEVSSLTCDALTELLAKITNTDVDCLKACQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 NIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEGLRK--EKVIGCYQLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 KYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ---IKPQELLEWELVVLGKLKWNLAAVTPHDFIEHILRKLPQQREKLSLIRKHAQTFIAL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 EEVFPLAMNYLDRFLAGVPTPKSH----LQLLGAVCMFLASKLKETSPLTAEKLCIYTDNS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 PPGLAMELLCHEVDP-VRREERYLPQCSYFKCVQ-KDIQPYMRRMVATWMLEVCEEQKCE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 PPSPTTE-DCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 10.1%; Score 177.5; DB 3; Length 309; Local Similarity 25.6%; Pred. No. 4.3e-12; les 69; Conservative 43; Mismatches 139; Indels 19
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REFERENCE/DOCKET NUMBER: MII-004C
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                                                                                    COUNTRY:
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227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9305000 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 LDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 LPETNGWPLQLVSVACLSLAAKMEE--PLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 YRQDQRDGSKS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0: FILING DATE: 16-OCT-1992
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SOFTWARE: ASCII(text)
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                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                         CITY:
                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 EERYLPQCSYFKCVQ-KDIQPYMRRMVATWMLEVCEEQKCEEEVFPLAMNYLDRFLAGVP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 ERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRR 116
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OPERATING SYSTEM:
                                                                                                                                                           ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGAAICGLQQDEEVSSLTCDALTELLAKITNTDVDCLKACQE-----QIEAVLLNSLQQ 260
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PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE TITLE OF INVENTION: REGULATORY PROTEINS
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                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PILING DATE: 19930525
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Rao, Ramachandra N.
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26.3%; Pred. No. 5e-
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5e-12;
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,1
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 PHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAA---VQ 245
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                                                               CLASSIFICATION:
                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                           CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                 STREET:
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63; Conservative
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Lilly Corporate Center/Patent Division
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  36,808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-947-120-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/07947120 Patent No. 5538846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEPHAX: 317-277-1917
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BC1-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,120
                               TELEPHONE: 415-777-9257
                                                                                                                                        APPLICATION NUMBER: US/0;
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 GLNLRSPNNFLSYYRLTRFLSRVIKC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 NWSVVKPENAESWCEGLR-KEKVIGC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 PHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAA---VQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 PLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 QLVSVACLSLAAKMEE--PLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                           NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Steuart Stre
STREET: Plaza
CITY: San Francisco
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 YLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 ISEEDLLVPRGSLLAMEHQLLCCEVETIRRAYPDANLLNDRV--LRAMLKAEETCAPSVS 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steuart Street Tower, 18th Fl., One Market
                 415-543-4219
                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                91-210-1
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SEQUENCE CHARACTERISTICS:

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Best Local Similarity
Matches 55; Conserv
                                                                                        141 ELLLVNKLKWNLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKFISNPP 200
                                                                                                                                                                                                                         110 RFLDSRRLPETNGWPLQLVSVACLSLAAKMEE--PLVPSLLDLQIEGAKY1FEPRTIRRM 167
201 SMVAAGSVVAA----VQGLNLRSPNNFLSYYRLTRFLSRVIKC 239
                                            228 SCIAAAAILTAANEIPNWSVVKPENAESWCEGLR-KEKVIGC 268
                                                                                                                                168 ELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFIRFLISRATEIIVSNIQEASFLAYWP 227
                                                                                                                                                                            87 RFLSLEPVKKSR---LQLLGATCMFVASKMKETIPLTAEKLCIYTDNS---IRPEBLLQM 140
                                                                                                                                                                                                                                                                   28 LRAMLKAEETCAPSVSYFKCVQKEVL-PSMRKIVATWMLEVCEEQKCEEEVFPLAMNYLD 86
                                                                                                                                                                                                                                                                                                               50 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                              9.8%; Score 171.5; DB 24.8%; Pred. No. 2e-11;
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Search completed: October 23, 2002, 14:39:51 Job time: 14 secs